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OM nucleic - nucleic search, using sw model

Run on: December 22, 2003, 16:07:12 ; Search time 357 Seconds  
(without alignments)  
8672.984 Million cell updates/sec

Title: US-10-049-742-22  
Perfect score: 1147  
Sequence: 1 gccttggtcaagcagaata.....gcctcctgagtagctggat 1147

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 19Jun03.\*

Rank	ID	Length	DB	Description
1	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*	1147	22	Nucleotide sequenc
2	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*	1096	22	Human cDNA sequenc
3	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*	1096	22	Human cDNA sequenc
4	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*	994	24	Nucleotide sequenc
5	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*	634	24	Human cDNA sequenc
6	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*	634	24	Human cDNA sequenc
7	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*	634	24	Human cDNA sequenc
8	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*	453	22	DNA encoding novel
9	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*	453	22	Human reproductive
10	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*	1147	22	Nucleotide sequenc
11	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*	1096	22	Human cDNA sequenc
12	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*	994	24	Nucleotide sequenc
13	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*	634	24	Human cDNA sequenc
14	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*	634	24	Human cDNA sequenc
15	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*	634	24	Human cDNA sequenc
16	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*	634	24	Human cDNA sequenc
17	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*	634	24	Human cDNA sequenc
18	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*	634	24	Human cDNA sequenc
19	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*	634	24	Human cDNA sequenc
20	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*	634	24	Human cDNA sequenc
21	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*	634	24	Human cDNA sequenc
22	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2001.DAT.*	634	24	Human cDNA sequenc
23	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*	634	24	Human cDNA sequenc
24	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*	634	24	Human cDNA sequenc
25	/SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2004.DAT.*	634	24	Human cDNA sequenc

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1147	100.0	1147	22	AAF54994
2	1096	95.6	2279	24	ABL55088
3	994	86.7	3286	24	ABL56700
4	634	55.3	754	20	AA234492
5	634	55.3	754	24	ABX04184
6	634	55.3	754	24	ABX76460
7	453	39.5	7453	22	AAS30481
8	453	39.5	7453	22	AAL06261

Rank	ID	Length	DB	Description	
9	450	39.2	747	22	AAI96802
10	258	22.5	884	24	ABL55114
11	145	12.6	2277	22	AAK68770
12	130	11.3	339	24	ABL5522
13	108	9.4	256	24	ABQ56856
14	89	7.8	11674	21	AA236210
15	89	7.8	12119	22	AA236196
16	89	7.8	12578	21	AA236196
17	89	7.8	12734	24	ABA95615
18	89	7.8	12842	21	AA236203
19	89	7.8	13198	21	AA236211
20	89	7.8	14078	21	AA338807
21	89	7.8	14578	21	AA248136
22	89	7.8	15065	21	AA236195
23	89	7.8	16622	21	AA236212
24	79	6.9	330	16	AAT24617
25	44	3.8	72604	20	ABK43231
26	44	3.8	72604	24	AA210752
27	42	3.7	5862	22	AA204575
28	42	3.7	5862	23	ABU97582
29	42	3.7	28001	24	ABS4410
30	42	3.7	28001	25	ABX93300
31	42	3.7	32249	22	AA204576
32	42	3.7	32249	23	ABU97583
33	42	3.7	35959	22	AAK78275
34	41	3.6	428	23	ABV05272
35	40	3.5	1116	24	ABK36123
36	40	3.5	1650	21	AA21035
37	40	3.5	1650	21	AA234913
38	40	3.5	13548	21	AA221037
39	40	3.5	13548	21	AA234915
40	40	3.5	22095	24	ABK84798
41	39	3.4	267	24	ABV98317
42	39	3.4	431	24	ABU67608
43	39	3.4	436	23	AA257509
44	39	3.4	445	22	AA25436
45	39	3.4	458	22	AA207690

#### ALIGNMENTS

RESULT 1  
AAF54994  
ID AAF54994 standard; DNA; 1147 BP.  
XX AAF54994;  
AC AAF54994;  
XX AAF54994;  
DT 15-MAY-2001 (first entry)  
XX Nucleotide sequence of a human chaperone polypeptide.

Human; chaperone polypeptide; reproductive disease; prolactin production; infertility; tumour; cancer; Peyronie's disease; eye disorder; glaucoma; conjunctivitis; keratitis; neuromuscular disorder; cystic fibrosis; metabolic disorder; Zellweger syndrome; Addison's disease; iritis; autoimmune disorder; inflammatory disorder; systemic lupus erythematosus; acquired immunodeficiency syndrome; AIDS; asthma; atherosclerosis; cell proliferative disorder; gene therapy; ss.

XX Homo sapiens.

Key	Location/Qualifiers
CDS	98..907
FT	/*tag= a
FT	/product= "chaperone protein"

WO200109178-A2.

06-FEB-2001.

03-AUG-2000; 2000WO-US21313.

PR 03-AUG-1999; 99US-0146908.  
PR 22-OCT-1999; 99US-0160924.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Yue H, Bandman O, Tang YT, Baughn MR, Azimzai Y, Lu DAM;  
XX WPI; 2001-159853/16.  
DR P-PSDB; AAB67455.  
XX New human chaperone proteins and polynucleotides, useful in diagnosing,  
XX treating and preventing reproductive, eye, neuromuscular, metabolic,  
XX autoimmune or inflammatory disorders  
XX Claim 5; Page 95-96; 102pp; English.  
XX The present sequence encodes a human chaperone polypeptide. Human  
XX chaperone polypeptides and polynucleotides are useful in the diagnosis,  
XX treatment and prevention of reproductive (e.g. prolactin production,  
XX infertility, endometrial or ovarian tumour, cancer of the breast,  
XX prostate or testis, Peyronie's disease), eye (e.g. conjunctivitis,  
XX keratitis, iritis, glaucoma), neuromuscular, metabolic (e.g. Zellweger  
XX syndrome, Addison's disease, cystic fibrosis), and autoimmune and  
XX inflammatory disorders (e.g. systemic lupus erythematosus, acquired  
XX immunodeficiency syndrome (AIDS), asthma, atherosclerosis), infectious  
XX or viral diseases, and cell proliferative disorders. Chaperone  
XX polynucleotides may be used for somatic or germline gene therapy, to  
XX detect and quantify gene expression in biopsied tissues in which  
XX expression is correlated with disease.  
XX Sequence 1147 BP; 287 A; 278 C; 314 G; 268 T; 0 other;  
SQ Query Match 100.0%; Score 1147; DB 22; Length 1147;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCCTTGGGTCAAGCAGATATTAAATAGGAGGGAATGACCTGTAGTGGCGGTA 60  
DB 1 GCCTTGGGTCAAGCAGATATTAAATAGGAGGGAATGACCTGTAGTGGCGGTA 60  
QY 61 CTGCCAGCTGAAGAGGAGTGGCTGACTCTTGACCATGGCTGGGGTTCCTGAGGATGA 120  
DB 61 CTGCCAGCTGAAGAGGAGTGGCTGACTCTTGACCATGGCTGGGGTTCCTGAGGATGA 120  
QY 121 GCTAAACCCCTTCCATGTACTGGGGTGTAGGCCACAGCATCAGATGTTGAATGAAGAA 180  
DB 121 GCTAAACCCCTTCCATGTACTGGGGTGTAGGCCACAGCATCAGATGTTGAATGAAGAA 180  
QY 181 GGCCCTATAGACAGCTGGCAGTGTGTTTCATCTCGACAAAATCATCATCCCGGCTGA 240  
DB 181 GGCCCTATAGACAGCTGGCAGTGTGTTTCATCTCGACAAAATCATCATCCCGGCTGA 240  
QY 241 GGAGGCTTCAAGGTTTGGGAGCAGCTTGGGACATTTGTCAGCAATGCTGAAAGCGAAA 300  
DB 241 GGAGGCTTCAAGGTTTGGGAGCAGCTTGGGACATTTGTCAGCAATGCTGAAAGCGAAA 300  
QY 301 GGAGTATGAGATGAACCAATGCGAGAGATGCTGAGCGGTCAGTAAATGAGTTTCT 360  
DB 301 GGAGTATGAGATGAACCAATGCGAGAGATGCTGAGCGGTCAGTAAATGAGTTTCT 360  
QY 361 GTCCAAAGCTGAGATGACCTCAAGGAGGCAATGAAATGATGTTAGCCGATGCCA 420  
DB 361 GTCCAAAGCTGAGATGACCTCAAGGAGGCAATGAAATGATGTTAGCCGATGCCA 420  
QY 421 AGGAAGCATAGAGGTTTGAATGAGCGGGAACCTAAGAGTGCAGATGCTGTGCTGA 480  
DB 421 AGGAAGCATAGAGGTTTGAATGAGCGGGAACCTAAGAGTGCAGATGCTGTGCTGA 480  
QY 481 GTGTAATAGGCTGCATCTCTGCTGAGAGGAGATTTGGGAGAGTCAAGCATGTTGG 540  
DB 481 GTGTAATAGGCTGCATCTCTGCTGAGAGGAGATTTGGGAGAGTCAAGCATGTTGG 540  
QY 541 CCTCAAGATCACCTACTTTTGCACATGATGATGGAAGGTTGATGACATCACAGAGTGGGC 600

DB 541 CCTCAAGATCACCTACTTTTGCACATGATGGATGGAAGGTTGATGACATCACAGAGTGGGC 600  
QY 601 TGGATGCCAGCGTGTAGGTATCTCCCCAGATATCCCAAGAGTCCCAATCATCATCTCAAT 660  
DB 601 TGGATGCCAGCGTGTAGGTATCTCCCCAGATATCCCAAGAGTCCCAATCATCTCAAT 660  
QY 661 TGGTCTTCGGATTTCCAGGACACAGAGGCGGAGAGCCACCCAGATGCCCTCTCTGC 720  
DB 661 TGGTCTTCGGATTTCCAGGACACAGAGGCGGAGAGCCACCCAGATGCCCTCTCTGC 720  
QY 721 TGAATCTTCAGATTTCTTGAATCGGATCTTCAAGTACCCCGGAGAGTGGCCAAATGG 780  
DB 721 TGAATCTTCAGATTTCTTGAATCGGATCTTCAAGTACCCCGGAGAGTGGCCAAATGG 780  
QY 781 GAACTTTCTTTCAGCTCTCTCAGCTGCTGCGCTGCGGAGCGCTGACGCTCTAAGCCCAACAG 840  
DB 781 GAACTTTCTTTCAGCTCTCTCAGCTGCTGCGCTGCGGAGCGCTGACGCTCTAAGCCCAACAG 840  
QY 841 CACAGTACCCCAAGGAGAGGAGCAAACTTAAGCGGCGGAGAAAGTGAAGAGGCGCTTCCA 900  
DB 841 CACAGTACCCCAAGGAGAGGAGCAAACTTAAGCGGCGGAGAAAGTGAAGAGGCGCTTCCA 900  
QY 901 AGCTTGTAGTCCCTCTCTCTTCTTCTCAATCAATGTGAGGAGTCAAAAGGCGCTGTAGCAC 960  
DB 901 AGCTTGTAGTCCCTCTCTCTTCTTCTCAATCAATGTGAGGAGTCAAAAGGCGCTGTAGCAC 960  
QY 961 AGSAGTGGATTTGATTTATCTCTCCCTCCCAACACCTAGGAACTGAAATCTTTTCTTTT 1020  
DB 961 AGSAGTGGATTTGATTTATCTCTCCCTCCCAACACCTAGGAACTGAAATCTTTTCTTTT 1020  
QY 1021 TATTTTGTAGATGGAGTCTTGTCTGTTGCCAGCTGGAGTGCAGTGTGTGATCTCAG 1080  
DB 1021 TATTTTGTAGATGGAGTCTTGTCTGTTGCCAGCTGGAGTGCAGTGTGTGATCTCAG 1080  
QY 1081 CTACTGCAACCTCTGTCTCCCGGTTCAAGCAATCTCCCATCTCAGCCTCTCTGAGTAG 1140  
DB 1081 CTACTGCAACCTCTGTCTCCCGGTTCAAGCAATCTCCCATCTCAGCCTCTCTGAGTAG 1140  
QY 1141 CTGGGAT 1147  
DB 1141 CTGGGAT 1147  
RESULT 2  
ABL55088 standard; DNA; 2279 BP.  
ID ABL55088 standard; DNA; 2279 BP.  
XX ABL55088;  
XX 08-OCT-2002 (first entry)  
XX Human cDNA sequence #1 from clone HNTPB82.  
XX Human; HNTPB82; secreted protein; immunosuppressive; food preservative;  
XX antithrombotic; antirheumatic; antiproliferative; cytostatic; cardiac;  
XX vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;  
XX virucide; fungicide; ophthalmological; vulnerary; gene therapy; ELISA;  
XX radioimmunoassay; enzyme linked immunosorbent assay; autoimmune disease;  
XX hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
XX cerebrovascular disorder; nervous system disorder; ocular disorder;  
XX wound healing; food additive; ss.  
XX Homo sapiens.  
XX Location/Qualifiers  
XX Key 36..1274  
XX CDS /\*tag= a  
XX FT 36..38  
XX FT sig\_peptide /\*tag= b  
XX FT mat\_peptide 39..1271  
XX FT /\*tag= c

PN WO200222638-A1.  
XX 21-MAR-2002.  
XX 17-JAN-2001; 2001WO-US01386.  
XX 12-SEP-2000; 2000US-232104P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;  
PI Ni J;  
XX WPI; 2002-258041/30.  
DR P-PSDB; ABB77019.  
XX  
XX New nucleic acid molecules encoding 22 human secreted proteins for  
PT diagnosing or treating e.g. autoimmune diseases, hyperproliferative  
PT disorders, and cardiovascular disorders, and used as food additives or  
PT preservatives -  
XX  
PS Disclosure; Page 451-452; 526pp; English.  
XX  
XX The sequence represents a cDNA sequence of the invention, isolated  
CC from human clone ID HNPB82. The invention relates to novel  
CC isolated nucleic acid molecules encoding 22 human secreted proteins. The  
CC proteins of the invention have immunosuppressive, antiarthritic,  
CC antirheumatic, antiproliferative, cytostatic, cardiant, vasotropic,  
CC cerebroprotective, nootropic, neuroprotective, antibacterial, virucide,  
CC fungicide, ophthalmological, and vulnerary activity. The polynucleotides  
CC may have a use in gene therapy. The polynucleotides and polypeptides  
CC encoded by them are used to prevent, treat or ameliorate a medical  
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
CC chickens or sheep. The polynucleotides and polypeptides are also used in  
CC diagnosing a pathological condition or susceptibility to a pathological  
CC condition. The antibodies to the proteins can also be used in alleviating  
CC symptoms associated with the disorders and in diagnostic immunoassays  
CC e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA).  
CC Disorders which are diagnosed or treated include autoimmune diseases,  
CC hyperproliferative disorders, cardiovascular disorders, cerebrovascular  
CC disorders, angiogenesis, nervous system disorders, infections caused by  
CC bacteria, viruses and fungi and ocular disorders. The polypeptides can  
CC also be used to aid wound healing and epithelial cell proliferation. The  
XX polypeptides can also be used as a food additive or preservative.  
XX  
SQ Sequence 2279 BP; 540 A; 518 C; 507 G; 614 T; 0 other;  
  
Query Match 95.6%; Score 1096; DB 24; Length 2279;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1146; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 GCCTTGGTCAAGCAGAAATATTATAGCGGGGAATGCACCTGTAGCTAGTGGGCGTA 60  
Db 368 GCCTTGGTCAAGCAGAAATATTATAGCGGGGAATGCACCTGTAGCTAGTGGGCGTA 427  
Qy 61 CTGCGACCGCTGACGAGGAAGTGGCTCGACTCTTCACCATGCTGGGGTTCTGAGGATGA 120  
Db 428 CTGCGACCGCTGACGAGGAAGTGGCTCGACTCTTCACCATGCTGGGGTTCTGAGGATGA 487  
Qy 121 GCTAAACCCCTTTCCATGTAAGTGGGGTTGAGGGCCACAGCATCAGATGTTCAACTGAAGAA 180  
Db 488 GCTAAACCCCTTTCCATGTAAGTGGGGTTGAGGGCCACAGCATCAGATGTTCAACTGAAGAA 547  
Qy 181 GGCCCTATAGACAGCTGCGAGTGTGTTTCATCTTCCTGACAAATAATCATCATCCCCGGGCTGA 240  
Db 548 GGCCCTATAGACAGCTGCGAGTGTGTTTCATCTTCCTGACAAATAATCATCATCCCCGGGCTGA 607  
Qy 241 GGAGGCTTCAAGTGTGGAGCAGCTTGGGACATGTGAGCAATGCTGAAAGGCGAA 300  
Db 608 GGAGGCTTCAAGTGTGGAGCAGCTTGGGACATGTGAGCAATGCTGAAAGGCGAA 667  
Qy 301 GGAGTATGAGATGAAACGAATGGCAGAGATGAGCTGAGCGGCTCAGTAAATGAGTTTCT 360

## RESULT 3

ABL56700

ID ABL56700 standard; cDNA; 3286 BP.

XX

AC ABL56700;

XX

DT 30-JUL-2002 (first entry)

XX

DE Nucleotide sequence of human P125-77.22 polypeptide.

XX

KW Human; P125-77.22; mucosal disease; BVDV infection; gene therapy;

KW Gene; ss.

XX

QY	541	CCTCAAGATCACCTACTTTGCACTGATCGAAGAAGGTGTATGACATCACAAGTGGGC	800
DB	1864	CCTCAAGATCACCTACTTTGCACTGATCGAAGAAGGTGTATGACATCACAAGTGGGC	1923
QY	601	TGGATGCCAGCGTGTAAGTATCTCCACAGATACCCACAGAGTCCCCATCACAATCATTCATT	660
DB	1924	TGGATGCCAGCGTGTAAGTATCTCCACAGATACCCACAGAGTCCCCATCACAATCATTCATT	1983
QY	661	TGTTCTCGGAATCCAGGCCACAGAGCGCGGCGAGAGCCACCCAGATGCCCGCTCTGCG	720
DB	1984	TGTTCTCGGAATCCAGGCCACAGAGCGCGGCGAGAGCCACCCAGATGCCCGCTCTGCG	2043
QY	721	TGATCTTCAGGATTTCTTTGAGTCGGATCTTTCAAGTAGTCCCAGGGCAGATGCCCAATGG	780
DB	2044	TGATCTTCAGGATTTCTTTGAGTCGGATCTTTCAAGTAGTCCCAGGGCAGATGCCCAATGG	2103
QY	781	GAACTTCTTTTCAGCTCCTCAGCCTGCCCCCTGGAGCCGCTGCAGCGCTCTAAGGCCCAACAG	840
DB	2104	GAACTTCTTTTCAGCTCCTCAGCCTGCCCCCTGGAGCCGCTGCAGCGCTCTAAGGCCCAACAG	2163
QY	841	CACAGTACCAGGAGAGAACCCAAACCTAAGCGCGGAAGAAAGTGAGGAGGCCCTTCCA	900
DB	2164	CACAGTACCAGGAGAGAACCCAAACCTAAGCGCGGAAGAAAGTGAGGAGGCCCTTCCA	2223
QY	901	ACGTTGATGCCCTTCTCTTTCTCAAATCAATGTCAAGGAGTCAAAGGGCTGTAGCAC	960
DB	2224	ACGTTGATGCCCTTCTCTTTCTCAAATCAATGTCAAGGAGTCAAAGGGCTGTAGCAC	2283
QY	961	AGGATGGAGTTGATTTATCCCTCTCCGCCAACACCTAGGAAGTGAATCTTTTTCTTTT	1020
DB	2284	AGGATGGAGTTGATTTATCCCTCTCCGCCAACACCTAGGAAGTGAATCTTTTTCTTTT	2343
QY	1021	TATTTTGTAGATGGAGTGTGCTCTGTGCCCCAGCTGGAGTGGTGTGATCTCAG	1080
DB	2344	TATTTTGTAGATGGAGTGTGCTCTGTGCCCCAGCTGGAGTGGTGTGATCTCAG	2403
QY	1081	CTTACTGCACCTCTGCTCTCCCGGGTTCAAGCAATTTCTCCATCTCAGCTCCTGAGTAG	1140
DB	2404	CTTACTGCACCTCTGCTCTCCCGGGTTCAAGCAATTTCTCCATCTCAGCTCCTGAGTAG	2463
QY	1141	CTGGGAT 1147	
DB	2464	CTGGGAT 2470	
 RESULT 4 AAZ34492 ID AAZ34492 standard; cDNA; 754 BP. XX AC AAZ34492; XX DT 01-FEB-2000 (first entry) XX DE Human LYST interacting protein LIP6 cDNA. XX KW LIP6; human; LYST-2; LYST interacting protein; lysosome; CHS; KW Chediak-Higashi syndrome; autoimmune disease; rheumatoid arthritis; KW systemic lupus erythematosus; inflammatory bowel disease; KW diabetes mellitus; multiple sclerosis; atopic disease; asthma; KW hay fever; rhinitis; urticaria; nasal polyp; cancer; KW neurodegenerative disease; pigmentation disorder; viral disease; KW platelet dysfunction; ss. XX OS Homo sapiens. XX FH Key Location/Qualifiers FT CDS 11..586 FT /tag= a FT /partial XX PN MO9951741-A2. XX			

PD 14-OCT-1999.

XX 29-MAR-1999; 98WO-US06831.

PF 03-APR-1998; 98US-0054956.

PR (CURA-) CURAGEN CORP.

PA Nandabalan K, Kingsmore S;

PI WPI; 1999-620203/53.

DR P-PSDB; AAY32126.

XX Protein complexes, interacting proteins, and related polynucleotides useful for treating and preventing e.g. atopie, autoimmune or neurodegenerative diseases -

PS Claim 21; Fig 7; 172pp; English.

XX This is the nucleotide sequence of cDNA which codes for a novel human LYST interacting protein, LIP6 (see AAY32126), that shows homology to pestivirus NS2-3. LYST is the human lysosomal Chediak-Higashi syndrome (CHS) protein. The invention relates to complexes of LYST or LYST-2 (see AAY32120) with proteins identified as interacting with LYST or LYST-2 by a modified yeast two-hybrid assay system. The interacting proteins include 10 novel proteins, LIP1-10 (see AAY32121-30). Methods of screening the protein complexes for efficacy in treating and/or preventing atopie diseases (e.g. asthma, nasal polyps, hay fever, rhinitis, urticaria) autoimmune diseases (e.g. CHS, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, diabetes mellitus, multiple sclerosis), neurodegenerative disease, certain forms of cancer, pigmentation disorders, platelet dysfunction and viral diseases are provided. Nucleic acids (see AAY34487-96) encoding LIP1-10, modulation of LIP function by gene therapy, use of antisense oligonucleotides for suppression of LIP protein expression, screening for agonists and antagonists, diagnosing or screening for the presence of a predisposition to a disease or disorder, and animal models are also disclosed.

XX Sequence 754 BP; 193 A; 185 C; 200 G; 176 T; 0 other;

SQ

Query Match 55.3%; Score 634; DB 20; Length 754;  
Best Local Similarity 99.9%; Pred. No. 1.9e-298;  
Matches 754; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 301 GGAGTATGAGTGAACGAGTGGCAGAGTAACTGAGTGGCGGTGAGTAACTGATTTCT 360

DB 1 GGAGTATGAGTGAACGAGTGGCAGAGTAACTGAGTGGCGGTGAGTAACTGATTTCT 60

QY 361 GTCCAAAGCTGCAAGTACCTCAAGGAGGCAATGATGATGTCGCGGATGCCA 420

DB 61 GTCCAAAGCTGCAAGTACCTCAAGGAGGCAATGATGATGTCGCGGATGCCA 120

QY 421 AGGAAGCATAGGAGGTTTGAATGACCGGGAACCTAAGAGTGCAGATCTGTGCTGA 480

DB 121 AGGAAGCATAGGAGGTTTGAATGACCGGGAACCTAAGAGTGCAGATCTGTGCTGA 180

QY 481 GTGTAAATAGGCTGCATCTGCTGAGGAAGGAGACTTTTGGGCGAGTCAAGCATTTGGG 540

DB 181 GTGTAAATAGGCTGCATCTGCTGAGGAAGGAGACTTTTGGGCGAGTCAAGCATTTGGG 240

QY 541 CCTCAAGATCACCTATTGCTGCTGATGGAAGGAGTGTATGATCACTCAGAGTGGGC 600

DB 241 CCTCAAGATCACCTATTGCTGCTGATGGAAGGAGTGTATGATCACTCAGAGTGGGC 300

QY 601 TGGATGCGAGGCTGTAGTATCTCCCGAGATACCCACAGAGTCCCTATCATCTCATT 660

DB 301 TGGATGCGAGGCTGTAGTATCTCCCGAGATACCCACAGAGTCCCTATCATCTCATT 360

QY 661 TGGTTCTCGGATTTCCAGGACCCAGAGGCGGCGAGAGCCACCCCGAGATGCCCTCTGC 720

DB 361 TGGTTCTCGGATTTCCAGGACCCAGAGGCGGCGAGAGCCACCCCGAGATGCCCTCTGC 420

QY 721 TGATCTTCAGGATTTCTTGATCGGATCTTTCAAGTACCCCGAGGCGAGATGCCATGG 780

DB 421 TGATCTTCAGGATTTCTTGATCGGATCTTTCAAGTACCCCGAGGCGAGATGCCATGG 479

QY 781 GAACTCTTTTGAGCTCCTCAGCTGCGCCCTGAGCGGCTGAGCCTCTAAGGCCCAACAG 840

DB 480 GAACTCTTTTGAGCTCCTCAGCTGCGCCCTGAGCGGCTGAGCCTCTAAGGCCCAACAG 539

QY 841 CACAGTACCCCAAGGAGAGCCCAAACTAAGCGGCGGGAAGAGTGAAGAGGCGCTTCCA 900

DB 540 CACAGTACCCCAAGGAGAGCCCAAACTAAGCGGCGGGAAGAGTGAAGAGGCGCTTCCA 599

QY 901 ACSTTGATGCGCCCTCTCTTTCTCAAAATCAATGTGAGGAGTCAAAAGGCTGTAGCAC 960

DB 600 ACSTTGATGCGCCCTCTCTTTCTCAAAATCAATGTGAGGAGTCAAAAGGCTGTAGCAC 659

QY 961 AGGATGAGTGTGATTTATCCCTCTCCCTCCCAACACTAGGAATCTGATCTTTTCTTT 1020

DB 660 AGGATGAGTGTGATTTATCCCTCTCCCTCCCAACACTAGGAATCTGATCTTTTCTTT 719

QY 1021 TATTTTGTGATGGAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1055

DB 720 TATTTTGTGATGGAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 754

RESULT 5

ABX04184

ID ABX04184 standard; cDNA; 754 BP.

XX AC ABX04184;

XX 10-JAN-2003 (first entry)

XX Human mRNA differentially expressed in mesenchymal cells #31.

XX Human; ss; gene; skeletal growth; cartilage degeneration disorder; chondroblastic phenotype; mesenchymal cell; cartilage formation; bone formation; arthritis; osteoarthritis; rheumatoid arthritis; gout arthritis; adjuvant arthritis; arthritis deformans; antigout; infectious arthritis; osteochondrosis; RDA; antiarthritic; osteopathic; antirheumatic; antiinflammatory; representational difference analysis.

XX Homo sapiens.

OS WO200271927-A2.

PN 19-SEP-2002.

XX 12-MAR-2002; 2002WO-US07787.

PF 12-MAR-2001; 2001US-274980P.

XX (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.

PA Yates KE, Mizuno S, Glowacki J;

PI WPI; 2002-723276/78.

DR New nucleic acid molecules capable of promoting chondrogenesis, useful for diagnosing and treating cartilaginous tissue degeneration, conditions, e.g. osteoarthritis, rheumatoid arthritis, gout arthritis, or osteochondrosis -

XX Claim 33; Page 129; 153pp; English.

XX The invention relates to new isolated nucleic acid molecule comprising a nucleic acid molecule consisting of a gene differentially expressed in cells undergoing differentiation from mesenchymal cell to a chondroblastic phenotype, or hybridising under stringent conditions to them (or their fragments). Also included are expression vectors, transformed host cells, expressed polypeptides or peptide fragments (which induce differentiation of a mesenchymal cell and may be used as an

immunogen ), binding partners of the polypeptides, a method for identifying an agent useful in modulating mesenchymal cell differentiation induction activity of a molecule, a method of diagnosing a condition characterised by aberrant expression of a nucleic acid molecule or its expression product; a method for determining regression, progression or onset of cartilaginous tissue degeneration condition in a subject characterised by aberrant expression of a nucleic acid molecule or its expression product, a method for treating a cartilaginous tissue degeneration condition, a method for treating a subject to reduce the risk of cartilaginous tissue degeneration condition developing in the subject, a method for identifying a candidate agent for treating a cartilaginous tissue degeneration condition, and a solid-phase nucleic acid molecule array consisting essentially of a set of nucleic acid molecule as cited above (or known from known genes shown to be differentially expressed in developing mesenchymal cells using the technique of representational difference analysis, RDA), its expression products or fragments, fixed to a solid substrate. The nucleic acids, polypeptides and agents are useful for treating cartilaginous tissue degeneration conditions such as osteoarthritis, rheumatoid arthritis, gout arthritis, adjuvant arthritis, arthritis deformans, infectious arthritis or osteochondrosis. The present sequence is a cDNA from a known gene differentially expressed in developing mesenchymal cells.

```
Query Match      55.3%; Score 634; DB 24; Length 754;
Best Local Similarity 99.9%; Pred. NO. 1.9e-298;
Matches 754; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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301	Qy	GGAGTATGAGATGAAACGAATGGCAGAGATGAGCTGAGCCGTCAGTAAATGAGTTCT	360
1	Db	GGAGTATGAGATGAAACGAATGGCAGAGATGAGCTGAGCCGTCAGTAAATGAGTTCT	60
361	Qy	GTCCAAAGCTGCAAGATGACCTCAAGGAGGCAATCAATACTATGATGTGTAGCCGATGCCA	420
61	Db	GTCCAAAGCTGCAAGATGACCTCAAGGAGGCAATCAATACTATGATGTGTAGCCGATGCCA	120
421	Qy	AGSAAAGCATAGAGAGTTTGAATATGGACCGGAACTTAAGAGTGCAGAGATCTGTCTGTA	480
121	Db	AGSAAAGCATAGAGAGTTTGAATATGGACCGGAACTTAAGAGTGCAGAGATCTGTCTGTA	180
481	Qy	GTGTANTAGGCTGCATCTCTGTGAGGAGGAGACTTTTGGCAGAGTCAAGCATGTTGGG	540
181	Db	GTGTANTAGGCTGCATCTCTGTGAGGAGGAGACTTTTGGCAGAGTCAAGCATGTTGGG	240
541	Qy	CCTCAAGATCACCTACTTTGGCACTGATGGATGGAAAGGTGTATGACATCACAGAGTGGGC	600
241	Db	CCTCAAGATCACCTACTTTGGCACTGATGGATGGAAAGGTGTATGACATCACAGAGTGGGC	300
601	Qy	TGATGCCAGCGTGTAGTATCTCCAGATATCCCAAGAGTCCCCTATCAATCTCATTT	660
301	Db	TGATGCCAGCGTGTAGTATCTCCAGATATCCCAAGAGTCCCCTATCAATCTCATTT	360
661	Qy	TGTTCTTCGGATTCAGAGCACAGAGGGCGGCAGAGGCCACCCAGATGSCCCTCCCTGC	720
361	Db	TGTTCTTCGGATTCAGAGCACAGAGGGCGGCAGAGGCCACCCAGATGSCCCTCCCTGC	420
721	Qy	TGATCTTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCCCCAGGGCAGATGCCCAATGG	780
421	Db	TGATCTTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCCCCAGGGCAGATGCCCAATGG	479
781	Qy	GAATCTTTTGAGCTCTCAGCTGCCCCCTGGAGCGCCTGCAGCCTCTTAAGCCCAACAG	840
480	Db	GAATCTTTTGAGCTCTCAGCTGCCCCCTGGAGCGCCTGCAGCCTCTTAAGCCCAACAG	539
841	Qy	CACAGTACCCAAGGGAGAGCCAAACCTTAAGCGCGGAAGAAAGTGAGGAGGCCCTTCCA	900
540	Db	CACAGTACCCAAGGGAGAGCCAAACCTTAAGCGCGGAAGAAAGTGAGGAGGCCCTTCCA	599
901	Qy	ACGTTGATGCCCTTCTCTTTCTCAAAATCAATGTCAAGGAGTCAAAAGGCTGTAGACAC	960
600	Db	ACGTTGATGCCCTTCTCTTTCTCAAAATCAATGTCAAGGAGTCAAAAGGCTGTAGACAC	659

	961	AGGATGGAGTTTGATTATTCCTCCTCCGCCAACACCTAGGAACCTGAATCTTTCCTTTT	1020
Qy			
Dd	660	AGGATGGAGTTTGATTATTCCTCCTCCGCCAACACCTAGGAACCTGAATCTTTCCTTT	719
Qy	1021	TATTTTTCGAGATGGAGTCTTGTCTGTGTGCCCG 1055	
Dd	720	TATTTTTCGAGATGGAGTCTTGTCTGTGTGCCCG 754	
RESULT 6			
ABS76460			
ID	ABS76460 standard; cDNA; 754 BP.		
XX	ABS76460;		
AC			
XX			
XX	11-DEC-2002 (first entry)		
XX			
DE	cDNA encoding human ovarian cancer marker OV38.		
XX			
KW	Human; ovarian cancer; marker; cancer; familial history; brain disorder;		
KW	central nervous system disorder; bacterial meningitis; viral meningitis;		
KW	Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;		
KW	brain herniation; inflammation; encephalitis; testicular disorder;		
KW	nontuberculous granulomatous orchitis; connective tissue disorder;		
KW	heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;		
KW	histological type; carcinogenic; ovarian cancer marker; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
XX	W0200271928-A2.		
PD	19-SEP-2002.		
XX			
Pf	14-MAR-2002; 2002WO-US07826.		
XX			
PR	14-MAR-2001; 2001US-2760295P.		
PR	14-MAR-2001; 2001US-276026P.		
PR	10-AUG-2001; 2001US-311732P.		
Pf	19-SEP-2001; 2001US-323580P.		
F.	26-SEP-2001; 2001US-324967P.		
PR	26-SEP-2001; 2001US-325102P.		
PR	26-SEP-2001; 2001US-325149P.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;		
PI	Meyers RE, Morrissey WP, Olandt PJ, Sen A, Vieby PO, Mills GB;		
PI	Bast RC, Lu K, Schmandt RE, Zhao X, Giatt K;		
XX			
DR	WPI; 2002-723277/78.		
DR	P-PDB; ABG96364.		
XX			
PT	Assessing whether a patient is afflicted with ovarian cancer, useful in		
PT	assessing the stage or progression of the disease, comprises comparing		
PT	the expression level of a cancer marker in a sample from a patient and		
PT	from a non cancer patient -		
XX			
PS	Disclosure; Page 300; 481pp; English.		
XX			
CC	The present invention relates to a new method for assessing whether a		
CC	patient is afflicted with ovarian cancer. The method involves comparing		
CC	the expression level of a marker in a patient sample and the normal level		
CC	of expression of the marker in a control non-ovarian cancer sample, where		
CC	the marker is selected from 363 cancer markers described in the		
CC	specification. The method of the invention is useful in diagnosing or		
CC	characterising cancer, in detecting the presence of cancer as early as		
CC	possible, and the recurrence of ovarian cancer. The method may also be of		
CC	particular use with patients having an enhanced risk of developing		
CC	ovarian cancer (e.g. patients having a familial history of ovarian		
CC	cancer). The cancer markers may be used in the management and treatment		
CC	of e.g. brain and central nervous system disorders (e.g. bacterial and		
CC	viral meningitis, Alzheimer's disease or Parkinson's disease), brain		
CC	disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),		

CC inflammations (e.g. bacterial or viral meningitis or encephalitis),  
CC testicular disorders (e.g. nontuberculous granulomatous orchitis),  
CC connective tissue disorders, or heart disorders (e.g. ischaemic heart  
CC disease or atherosclerosis). The compositions and methods may also be  
CC used in assessing the histological type of neoplasm associated with  
CC ovarian cancer, monitoring the progression of ovarian cancer,  
CC determining whether ovarian cancer has metastasized or is likely to  
CC metastasize, selecting a composition for inhibiting ovarian cancer,  
CC assessing the ovarian carcinogenic potential of a compound, or  
CC inhibiting ovarian cancer or at risk of developing ovarian cancer. The  
CC present nucleic acid sequence encodes one of the ovarian cancer markers  
CC described in the invention.

XX SQ Sequence 754 BP; 193 A; 185 C; 200 G; 176 T; 0 other;

Query Match 55.3%; Score 634; DB 24; Length 754;  
Best Local Similarity 99.9%; Pred. No. 1.9e-298;  
Matches 754; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	301	GGAGTATGAGATGAACGAATGGCAGAGATGACCTGAGCGGTCAATGATGTTCT	360
Db	1	GGAGTATGAGATGAACGAATGGCAGAGATGACCTGAGCGGTCAATGATGTTCT	60
Qy	361	GTCCAAAGCTGCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTGACCGGATG	420
Db	61	GTCCAAAGCTGCAAGATGACCTCAAGGAGGCAATGAATACTATGATGTGACCGGATG	120
Qy	421	AGGAAGCATAGGAGGTTTGAATGGACCGGAACTTAAGATGCCAGATACCTGTGCTGA	480
Db	121	AGGAAGCATAGGAGGTTTGAATGGACCGGAACTTAAGATGCCAGATACCTGTGCTGA	180
Qy	481	GTGTAATAGGCTGCATCCTCTGAGGAAGGAGACTTTGGCGAGAGTCAAGCATGTTGGG	540
Db	181	GTGTAATAGGCTGCATCCTCTGAGGAAGGAGACTTTGGCGAGAGTCAAGCATGTTGGG	240
Qy	541	CCTCAAGATCACCTTCTGCACTGATGGATGGAAAGTGTATGACATCAAGAGTGGGC	600
Db	241	CCTCAAGATCACCTTCTGCACTGATGGATGGAAAGTGTATGACATCAAGAGTGGGC	300
Qy	601	TGGATGCGAGGCTAGTATCTCCAGATACCCAGAGTCCCTATCACATCTCAT	660
Db	301	TGGATGCGAGGCTAGTATCTCCAGATACCCAGAGTCCCTATCACATCTCAT	360
Qy	661	TGGTCTCGGATTCAGGACCCAGAGGCGGAGAGCCACCCAGATGCCCTCTCTGC	720
Db	361	TGGTCTCGGATTCAGGACCCAGAGGCGGAGAGCCACCCAGATGCCCTCTCTGC	420
Qy	721	TGATCTTTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCCCGGAGAGTGCCTATGG	780
Db	421	TGATCTTTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCCCGGAGAGTGCCTATGG	479
Qy	781	GAACTCTTTGCACTCTCTCAGCTGCGCTGGAGCGCTGCGAGCTCTAAGGCCAACAG	840
Db	480	GAACTCTTTGCACTCTCTCAGCTGCGCTGGAGCGCTGCGAGCTCTAAGGCCAACAG	539
Qy	841	CACAGTACCAAGGAGAGCCAAACCTAAGCGGCGGAGAAAGTGAAGGCGCTTCCA	900
Db	540	CACAGTACCAAGGAGAGCCAAACCTAAGCGGCGGAGAAAGTGAAGGCGCTTCCA	599
Qy	901	ACGTTGATGCGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	960
Db	600	ACGTTGATGCGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	659
Qy	961	AGGATGAGGTTGATTTATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1020
Db	660	AGGATGAGGTTGATTTATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	719
Qy	1021	TATTTTGTAGATGGAGTCTTGCTCTGTTGCCAG 1055	
Db	720	TATTTTGTAGATGGAGTCTTGCTCTGTTGCCAG 754	

RESULT 7

PR	08-SEP-2000;	2000US-0231242.	PR	17-NOV-2000;	2000US-0249245.
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PR	08-SEP-2000;	2000US-0231413.	PR	17-NOV-2000;	2000US-0249297.
PR	08-SEP-2000;	2000US-0231414.	PR	17-NOV-2000;	2000US-0249299.
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PR	14-SEP-2000;	2000US-0232400.	PR	06-DEC-2000;	2000US-0251479.
PR	14-SEP-2000;	2000US-0232401.	PR	08-DEC-2000;	2000US-0251856.
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PR	29-SEP-2000;	2000US-0236367.	XX		
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PR	02-OCT-2000;	2000US-0237037.	XX		
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PR	02-OCT-2000;	2000US-0237040.	XX		
PR	13-OCT-2000;	2000US-0239935.	XX		
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PR	20-OCT-2000;	2000US-0241785.	XX		
PR	20-OCT-2000;	2000US-0241786.	XX		
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PR	20-OCT-2000;	2000US-0241808.	XX		
PR	20-OCT-2000;	2000US-0241809.	XX		
PR	01-NOV-2000;	2000US-0241826.	XX		
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PR	08-NOV-2000;	2000US-0244675.	XX		
PR	08-NOV-2000;	2000US-0244676.	XX		
PR	08-NOV-2000;	2000US-0244677.	XX		
PR	08-NOV-2000;	2000US-0244678.	XX		
PR	08-NOV-2000;	2000US-02446523.	XX		
PR	08-NOV-2000;	2000US-0244524.	XX		
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PR	08-NOV-2000;	2000US-0244526.	XX		
PR	08-NOV-2000;	2000US-0244527.	XX		
PR	08-NOV-2000;	2000US-0244528.	XX		
PR	08-NOV-2000;	2000US-0244532.	XX		
PR	08-NOV-2000;	2000US-0244609.	XX		
PR	08-NOV-2000;	2000US-0244610.	XX		
PR	08-NOV-2000;	2000US-0244611.	XX		
PR	08-NOV-2000;	2000US-0244613.	XX		
PR	17-NOV-2000;	2000US-0249207.	XX		
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PR	17-NOV-2000;	2000US-0249212.	XX		
PR	17-NOV-2000;	2000US-0249213.	XX		
PR	17-NOV-2000;	2000US-0249214.	XX		
PR	17-NOV-2000;	2000US-0249215.	XX		
PR	17-NOV-2000;	2000US-0249216.	XX		
PR	17-NOV-2000;	2000US-0249217.	XX		
PR	17-NOV-2000;	2000US-0249218.	XX		
PR	17-NOV-2000;	2000US-0249244.	XX		

Claim 1; SEQ ID No 339; 512pp; English.

The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prognosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, acute bacterial prostatitis, benign prostatic hyperplasia, granulomatous prostatitis, malacoplakia, benign prostatic hyperplasia or hyperplasia, and prostate neoplastic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. (I), (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anemia), hyperproliferative disorders, urinary system disorders (glomerulonephritis), cardiovascular disorders (arrhythmias), respiratory disorders, musculoskeletal system disorders, neural activity and neurological disorders (Alzheimer's disease and Parkinson's disease), endocrine disorders (Addison's disease), gastrointestinal disorders (inflammatory disorders), liver disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders, disorders of the large intestine, developmental and inherited disorders, diseases at the cellular level, and wound healing and epithelial cell proliferation. (I) or (II) is useful to prevent skin aging, for preventing hair loss, to maintain

Query Match 39.5%; Score 453; DB 22; Length 7453;  
Best Local Similarity 100.0%; Pred. No. 2.7e-210;  
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	695	AGAGCCACCCAGATGCCCTCTCTGCTGATCTTCAGGATTTCTTGATCGGATCTTCAA	754
Db	3315	AGAGCCACCCAGATGCCCTCTCTGCTGATCTTCAGGATTTCTTGATCGGATCTTCAA	3374
Qy	755	GTACCCCGAGGAGATGCCCAATGGAACTTTTTCAGCTCTCAGCTGCCCTGGA	814
Db	3375	GTACCCCGAGGAGATGCCCAATGGAACTTTTTCAGCTCTCAGCTGCCCTGGA	3434
Qy	815	GCCGCTGAGCTCTTAAGCCCAACAGCACAGTACCCAGGAGAGCAACCTAACGCG	874
Db	3435	GCCGCTGAGCTCTTAAGCCCAACAGCACAGTACCCAGGAGAGCAACCTAACGCG	3494
Qy	875	CGGAAGAAAGTGAGAGGCCCTTCCAACTGATGCCCTTCTTCTTCTCAATCAATG	934

Db 3495 CGGAGAAAGTGAGAGGCCCTTCACAGTTGATGCCCTTCTCTTTCTCAATCAATG 3554  
QY 935 TCAGGGAGTCAAAAGGGCTGTAGCACAGGATGGAGTTTGATTTATCCCTCTCTCCCAAC 994  
Db 3555 TCAGGGAGTCAAAAGGGCTGTAGCACAGGATGGAGTTTGATTTATCCCTCTCTCCCAAC 3614  
QY 995 ACCTAGGAACCTGAATCTTTTCTTTTATTTTGGATGGAGCTTGTCTGTGGCCA 1054  
Db 3615 ACCTAGGAACCTGAATCTTTTCTTTTATTTTGGATGGAGCTTGTCTGTGGCCA 3674  
QY 1055 GCTGAGTGCAGTGGTGTGATCTCAGCTTACTGCAACTCTGTCTCCGGGTTCAAGCA 1114  
Db 3675 GCTGAGTGCAGTGGTGTGATCTCAGCTTACTGCAACTCTGTCTCCGGGTTCAAGCA 3734  
QY 1115 TTCTCCCATCTCAGCTTCTCAGTGTGGAT 1147  
Db 3735 TTCTCCCATCTCAGCTTCTCAGTGTGGAT 3767

RESULT 8

AAI06261

ID AAI06261 standard; DNA; 7453 BP.

XX AAI06261;

AC AAI06261;

DT 21-NOV-2001 (first entry)

DE Human reproductive system related antigen DNA SEQ ID NO: 8949.

XX Human; reproductive system related antigen; reproductive system disorder;

KW cancer; gene therapy; ds.

XX Homo sapiens.

XX WO200155320-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01339.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209457.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

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PR 11-JUL-2000; 2000US-0217487.

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PR 14-AUG-2000; 2000US-0224518.

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PR 14-AUG-2000; 2000US-0225213.

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PR 14-AUG-2000; 2000US-0225270.

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PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

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PR 08-NOV-2000; 2000US-0246526.  
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PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.

17-NOV-2000;	2000US-0249208.	PR	3555	TCAGGAGTCAAAAGGGCTGTACACAGGATGGAGTTTGTATTATCCCTCTCCCTCCCAAC	3614
17-NOV-2000;	2000US-0249209.	PR	995	ACCTAGGAACCTGAATCTTTTCTTTTATTTTATTTTGTAGATGGAGTCTTGCTCTGTGGCCCA	1054
17-NOV-2000;	2000US-0249210.	PR	3615	ACCTAGGAACCTGAATCTTTTCTTTTATTTTATTTTGTAGATGGAGTCTTGCTCTGTGGCCCA	3674
17-NOV-2000;	2000US-0249211.	PR	1055	GCTGGAGTGCAGTGGTGTGATCTCAGCTTACTGCAACCTCTGTCTCCCGGGTTCAAGCAA	1114
17-NOV-2000;	2000US-0249212.	PR	3675	GCTGGAGTGCAGTGGTGTGATCTCAGCTTACTGCAACCTCTGTCTCCCGGGTTCAAGCAA	3734
17-NOV-2000;	2000US-0249213.	PR	1115	TTCTCCCATCTCAGCCTCCTCAGTAGCTGGAT	1147
17-NOV-2000;	2000US-0249214.	PR	3735	TTCTCCCATCTCAGCCTCCTCAGTAGCTGGAT	3767
17-NOV-2000;	2000US-0249215.	PR			
17-NOV-2000;	2000US-0249216.	PR			
17-NOV-2000;	2000US-0249217.	PR			
17-NOV-2000;	2000US-0249218.	PR			
17-NOV-2000;	2000US-0249219.	PR			
17-NOV-2000;	2000US-0249220.	PR			
17-NOV-2000;	2000US-0249221.	PR			
17-NOV-2000;	2000US-0249222.	PR			
17-NOV-2000;	2000US-0249223.	PR			
17-NOV-2000;	2000US-0249224.	PR			
17-NOV-2000;	2000US-0249225.	PR			
17-NOV-2000;	2000US-0249226.	PR			
17-NOV-2000;	2000US-0249227.	PR			
17-NOV-2000;	2000US-0249228.	PR			
17-NOV-2000;	2000US-0249229.	PR			
17-NOV-2000;	2000US-0249230.	PR			
17-NOV-2000;	2000US-0249231.	PR			
17-NOV-2000;	2000US-0249232.	PR			
17-NOV-2000;	2000US-0249233.	PR			
17-NOV-2000;	2000US-0249234.	PR			
17-NOV-2000;	2000US-0249235.	PR			
17-NOV-2000;	2000US-0249236.	PR			
17-NOV-2000;	2000US-0249237.	PR			
17-NOV-2000;	2000US-0249238.	PR			
17-NOV-2000;	2000US-0249239.	PR			
17-NOV-2000;	2000US-0249240.	PR			
17-NOV-2000;	2000US-0249241.	PR			
17-NOV-2000;	2000US-0249242.	PR			
17-NOV-2000;	2000US-0249243.	PR			
17-NOV-2000;	2000US-0249244.	PR			
17-NOV-2000;	2000US-0249245.	PR			
17-NOV-2000;	2000US-0249246.	PR			
17-NOV-2000;	2000US-0249247.	PR			
17-NOV-2000;	2000US-0249248.	PR			
17-NOV-2000;	2000US-0249249.	PR			
17-NOV-2000;	2000US-0249250.	PR			
17-NOV-2000;	2000US-0249251.	PR			
17-NOV-2000;	2000US-0249252.	PR			
17-NOV-2000;	2000US-0249253.	PR			
17-NOV-2000;	2000US-0249254.	PR			
17-NOV-2000;	2000US-0249255.	PR			
17-NOV-2000;	2000US-0249256.	PR			
17-NOV-2000;	2000US-0249257.	PR			
17-NOV-2000;	2000US-0249258.	PR			
17-NOV-2000;	2000US-0249259.	PR			
17-NOV-2000;	2000US-0249260.	PR			
17-NOV-2000;	2000US-0249261.	PR			
17-NOV-2000;	2000US-0249262.	PR			
17-NOV-2000;	2000US-0249263.	PR			
17-NOV-2000;	2000US-0249264.	PR			
17-NOV-2000;	2000US-0249265.	PR			
17-NOV-2000;	2000US-0249266.	PR			
17-NOV-2000;	2000US-0249267.	PR			
17-NOV-2000;	2000US-0249268.	PR			
17-NOV-2000;	2000US-0249269.	PR			
17-NOV-2000;	2000US-0249270.	PR			
17-NOV-2000;	2000US-0249271.	PR			
17-NOV-2000;	2000US-0249272.	PR			
17-NOV-2000;	2000US-0249273.	PR			
17-NOV-2000;	2000US-0249274.	PR			

Db 178 GCAATGCTGAAGCGAAAGAGATATGAGATGAACGAATGGCAGAGAAATGAGCTGAGCC 237  
Qy 342 GGTCAAGTAATGAGTTCTTCTTCAAGCTGCAAGATGACCTCAAGAGGCAATGAATACTA 401  
Db 238 GGTCAAGTAATGAGTTCTTCTTCAAGCTGCAAGATGACCTCAAGAGGCAATGAATACTA 297  
Qy 402 TGATGTTAGCCGATGCCAAGGAAAGCATAGGAGGTTTGAATGGACCGGAAACCTAAGA 461  
Db 298 TGATGTTAGCCGATGCCAAGGAAAGCATAGGAGGTTTGAATGGACCGGAAACCTAAGA 357  
Qy 462 GTGCCAGATAGTGTGCTGAGTGAATAGGCTGATCTGCTGAGGAAGGAGCTTTGGG 521  
Db 358 GTGCCAGATAGTGTGCTGAGTGAATAGGCTGATCTGCTGAGGAAGGAGCTTTGGG 417  
Qy 522 CAGAGTCAAGCATGTTGGGCTCAAGATCACTTGTGACATGATGGATGGAAGGTGT 581  
Db 418 CAGAGTCAAGCATGTTGGGCTCAAGATCACTTGTGACATGATGGATGGAAGGTGT 477  
Qy 582 ATGACATCACAGAGTGGGCTGGATGCCAGC 611  
Db 478 ATGACATCACAGAGTGGGCTGGATGCCAGC 507  
RESULT 10  
ABL55114  
ID ABL55114 standard; DNA; 884 Bp.  
XX AC ABL55114;  
XX 08-OCT-2002 (first entry)  
XX Human cDNA sequence #2 from clone HNTPB82.  
XX Human; HNTPB82; secreted protein; immunosuppressive; food preservative;  
KW antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;  
KW vasotropic; cerebrotective; nootropic; neuroprotective; antibacterial;  
KW virucide; fungicide; ophthalmological; vulnertary; gene therapy; ELISA;  
KW radioimmunoassay; enzyme linked immunosorbent assay; autoimmune disease;  
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
KW wound healing; food additive; ss.  
XX Homo sapiens.  
FH Key Location/Qualifiers  
CDS 272..883  
FT /\*tag= a  
FT /note= "No stop codon given"  
FT sig\_peptide 272..400  
FT /\*tag= b  
FT mat\_peptide 401..883  
FT /\*tag= c  
XX WO200222638-A1.  
XX 21-MAR-2002.  
XX 17-JAN-2001; 2001WO-US01386.  
XX 12-SEP-2000; 2000US-232104P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;  
PI Ni J;  
XX WPI; 2002-258041/30.  
DR P-PSDB; ABB77045.  
XX New nucleic acid molecules encoding 22 human secreted proteins for  
PT diagnosing or treating e.g. autoimmune diseases, hyperproliferative

PT disorders, and cardiovascular disorders, and used as food additives or  
PT preservatives -  
XX Disclosure; Page 466-467; 526pp; English.  
XX The sequence represents a cDNA sequence of the invention, isolated  
CC from human clone ID HNTPB82. The invention relates to novel  
CC isolated nucleic acid molecules encoding 22 human secreted proteins. The  
CC proteins of the invention have immunosuppressive, antirheumatic,  
CC antirheumatic, antiproliferative, cytostatic, cardiant, vasotropic,  
CC cerebrotective, nootropic, neuroprotective, antibacterial, virucide,  
CC fungicide, ophthalmological, and vulnerary activity. The polynucleotides  
CC may have a use in gene therapy. The polynucleotides and polypeptides  
CC encoded by them are used to prevent, treat or ameliorate a medical  
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
CC chickens or sheep. The polynucleotides and polypeptides are also used in  
CC diagnosing a pathological condition or susceptibility to a pathological  
CC condition. The antibodies to the proteins can also be used in alleviating  
CC symptoms associated with the disorders and in diagnostic immunoassays  
CC e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA).  
CC Disorders which are diagnosed or treated include autoimmune diseases,  
CC hyperproliferative disorders, cardiovascular disorders, cerebrovascular  
CC disorders, angiogenesis, nervous system disorders, infections caused by  
CC bacteria, viruses and fungi and ocular disorders. The polypeptides can  
CC also be used to aid wound healing and epithelial cell proliferation. The  
CC polypeptides can also be used as a food additive or preservative.  
XX  
XX Sequence 884 Bp; 187 A; 178 C; 291 G; 228 T; 0 other;  
Query Match 22.5%; Score 258; DB 24; Length 884;  
Best Local Similarity 100.0%; Pred. No. 2.5e-115; Indels 0; Gaps 0;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCCTTGGGTCAAGCAGAAATATTATAGCAGGGGAATGCACCTGTAGCTAGTGGCGCTA 60  
Db 562 GCCTTGGGTCAAGCAGAAATATTATAGCAGGGGAATGCACCTGTAGCTAGTGGCGCTA 621  
Qy 61 CTGCCAGCTCAAGAGGAAGTGGCTCGACTCTTGACCACTGGCTGGGGTTCCTGAGATGA 120  
[ 622 CTGCCAGCTCAAGAGGAAGTGGCTCGACTCTTGACCACTGGCTGGGGTTCCTGAGATGA 681  
Qy 121 GCTAAACCTTTCCCATGTACTGGGGTGGAGCCACAGCATCAGATGTTGAACCTGAAGAA 180  
Db 682 GCTAAACCTTTCCCATGTACTGGGGTGGAGCCACAGCATCAGATGTTGAACCTGAAGAA 741  
Qy 181 GGCCTATAGACAGCTGGCAGTGTGTTTCATCCTCACAATAATCATATCCCGGGCTGA 240  
Db 742 GGCCTATAGACAGCTGGCAGTGTGTTTCATCCTCACAATAATCATATCCCGGGCTGA 801  
Qy 241 GGAGGCCTTCAAGGTTTT 258  
Db 802 GGAGGCCTTCAAGGTTTT 819  
RESULT 11  
AAK68770  
ID AAK68770 standard; DNA; 2277 Bp.  
XX AC AAK68770;  
XX 06-NOV-2001 (first entry)  
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23582.  
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
XX Homo sapiens.  
XX WO200157182-A2.  
XX 09-AUG-2001.  
XX



PT useful for preventing, diagnosing and/or treating cancers and  
XX metastasis -  
PS Disclosure; SEQ ID NO 23582; 3071pp + Sequence Listing; English.  
XX  
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patient's own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/haematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/haematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention.  
XX  
SQ Sequence 2277 BP; 479 A; 579 C; 662 G; 557 T; 0 other;  
Query Match 12.6%; Score 145; DB 22; Length 2277;  
Best Local Similarity 100.0%; Pred. No. 2.7e-60; Indels 0; Gaps 0;  
Matches 145; Conservative 0; Mismatches 0;  
QY 1 GCCTGGGTCAAGCAGCAATATTATAGGAGGAGGGAATGCACCTGTAGTGGCGCTA 60  
DB 2133 GCCTGGGTCAAGCAGCAATATTATAGGAGGAGGGAATGCACCTGTAGTGGCGCTA 2192  
QY 61 CTGCCAGCCTGAAGAGGAGTGGCTCGACTCTTGACCATGGCTGGGTTCTTGAGGATGA 120  
DB 2193 CTGCCAGCCTGAAGAGGAGTGGCTCGACTCTTGACCATGGCTGGGTTCTTGAGGATGA 2252  
QY 121 GCTAAACCTTTCCATGTAAGTGGG 145  
DB 2253 GCTAAACCTTTCCATGTAAGTGGG 2277  
RESULT 12  
ID ABL85522 standard; cDNA; 339 BP.  
XX  
AC ABL85522;  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE Human ovarian cancer related cDNA clone SEQ ID NO:8500.  
XX  
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192581-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 29-MAY-2001; 2001WO-US17756.  
XX  
PR 26-MAY-2000; 2000US-207484P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Algate PA, Harlocker SL, Jones R;  
XX  
DR WPI; 2002-122075/16.  
XX  
PT Composition for therapy and diagnosis of ovarian cancer comprising  
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
PT polypeptide, antibody specific to polypeptide or T cell expressing

PT polypeptide -  
XX  
PS Claim 1; SEQ ID 8500; 489pp; English.  
XX  
CC The present invention describes a composition (I) comprising: carriers  
CC and immunostimulants; and a polypeptide (II) of a ovarian tumour  
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence  
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to  
CC ABL97934, (III) encoding (II) having a sequence (S2), a T cell  
CC population of (II), or antigen presenting cells that express (II).  
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to  
CC (S1) can be used for detecting ovarian cancer in a patient's biological  
CC sample preferably serum or ovarian tissue. The method comprises  
CC contacting a biological sample from a patient with (IV), detecting the  
CC amount of polynucleotide hybridising to (IV) and comparing the amount to  
CC a predetermined cutoff value and thereby detecting ovarian cancer in the  
CC patient, where the amount of polynucleotide hybridising to (IV) is  
CC detected preferably by polymerase chain reaction (PCR). (I) comprising  
CC (III) and/or (II) is useful for stimulating and/or expanding T cells  
CC specific for an ovarian tumour protein comprising contacting T cells  
CC with (III) or (II). (III) is useful in design and preparation of  
CC ribozyme molecules for inhibiting expression of the tumour polypeptides  
CC and proteins in tumour cells; and to isolate a full length gene from a  
CC suitable library e.g., a tumour cDNA library using well known  
CC techniques.  
XX  
SQ Sequence 339 BP; 73 A; 76 C; 67 G; 123 T; 0 other;  
Query Match 11.3%; Score 130; DB 24; Length 339;  
Best Local Similarity 100.0%; Pred. No. 5.6e-53;  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 899 CAACGTTGATGCCCTTCTCTTCTCAAAATCAATGTCAAGGAGTCAAAAGGCTGTAGC 958  
DB 26 CAACGTTGATGCCCTTCTCTTCTCAAAATCAATGTCAAGGAGTCAAAAGGCTGTAGC 85  
QY 959 ACAGATGGAGTTTGATTTATCCCTCTCCCCCAACCTAGGAACTGAAATCTTTTCTT 1018  
DB 86 ACAGATGGAGTTTGATTTATCCCTCTCCCCCAACCTAGGAACTGAAATCTTTTCTT 145  
QY 1019 TTTATTTTTT 1028  
DB 146 TTTATTTTTT 155  
RESULT 13  
ID ABL856856 standard; cDNA; 256 BP.  
XX  
AC ABL856856;  
XX  
DT 02-AUG-2002 (first entry)  
XX  
DE Human colon cancer related nucleotide sequence SEQ ID NO:551.  
XX  
KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;  
XX genetic analysis; diagnostic; antisense therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200229086-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 02-OCT-2001; 2001WO-US30732.  
XX  
PR 02-OCT-2000; 2000US-237271P.  
XX  
PA (FARB) BAYER CORP.  
XX  
PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;  
XX Thiagalingam A, Lewis ME;

DR WPI; 2002-426115/45.  
XX  
PT New isolated nucleic acid that is differentially expressed in cancer  
PT tissues useful for determining the presence of colon cancer in a cell  
PT or tissue type, and in antisense therapy -  
XX  
PS Claim 1; Fig 1; 796pp; English.  
XX  
CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially  
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins  
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be  
CC used in antisense therapy. An antibody immunoreactive with a polypeptide  
CC encoded by (I) is useful for detecting cancer in a patient sample, and  
CC for detecting the presence or absence of a polynucleotide encoded by a  
CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived  
CC from (I) can be used for determining the presence of a nucleic acid which  
CC hybridizes to (I), and for determining the phenotype of cells in a sample  
CC of cells from a patient. (I) is useful for determining the presence of  
CC colon cancer in a cell or tissue type, for determining the presence or  
CC state of other type of cancer, in antisense therapy, to generate  
CC macroarrays on a solid surface, to identify a chromosome on which the  
CC corresponding gene resides, and in tissue profiling, forensics, genetic  
CC analysis, mapping and diagnostic applications. (I) can be used to raise  
CC antibodies, and to screen for peptide analogues and antagonists.  
XX  
SQ Sequence 256 BP; 57 A; 64 C; 59 G; 70 T; 6 other;  
Query Match 9.4%; Score 108; DB 24; Length 256;  
Best Local Similarity 100.0%; Pred. No. 2.9e-42;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 872 CGCGGAGAAAGTGAAGAGGCGCTTCCAACTGATGCCCTTCTTTCTTCAATCA 931  
DB 26 CGGCGGAGAAAGTGAAGAGGCGCTTCCAACTGATGCCCTTCTTTCTTCAATCA 85  
QY 932 ATGTGAGGAGTCAAAAGGCTGTAGCACAGATGGAGTTGATTAT 979  
DB 86 ATGTGAGGAGTCAAAAGGCTGTAGCACAGATGGAGTTGATTAT 133  
RESULT 14  
AAZ36210  
ID AAZ36210 standard; DNA; 11674 BP.  
XX  
AC AAZ36210;  
XX  
DT 11-FEB-2000 (first entry)  
XX  
DE Nucleotide sequence of functional HCV-BVDV chimera from pCBV/p7.  
XX  
KW Pseudorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;  
KW 5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;  
KW bovine viral diarrhoea virus; NADL; vaccine; ss.  
XX  
OS Chimeric - Hepatitis C virus.  
OS Chimeric - Bovine viral diarrhoea virus.  
XX  
PN WO955366-A1.  
XX  
XX 04-NOV-1999.  
XX  
PF 23-APR-1999; 99WO-US08850.  
XX  
PR 24-APR-1998; 98US-0082964.  
XX  
XX (UNIW ) UNIV WASHINGTON.  
XX  
PI Rice CM, Frolov I, McBride MS;  
XX  
DR WPI; 2000-013359/01.  
XX  
PT Chimeric viral RNA, used in vaccine against BVDV -  
XX

PS Disclosure; Fig 22; 108pp; English.  
XX  
CC The present sequence represents a functional Hepatitis C virus  
CC (HCV)-bovine viral diarrhoea virus (BVDV) chimeric virus of the  
CC invention. The specification describes chimeric viral RNA comprising a  
CC 5' nontranslated region (5'NTR); an open reading frame (ORF) region;  
CC and a 3' NTR; where at least one of the regions is chimeric and  
CC comprises a nucleotide sequence from a pestivirus in operable linkage  
CC with a heterologous nucleotide sequence, preferably from HCV. The  
CC chimeric viral RNA is replication-competent. The chimeric viral RNA  
CC can be used in a method for identifying compounds having antiviral  
CC activity against HCV. When the pestivirus viral nucleotide sequence is  
CC from bovine viral diarrhoea virus (BVDV), the chimeric viral RNA can be  
CC used in a vaccine against BVDV.  
XX  
SQ Sequence 11674 BP; 3407 A; 2614 C; 3100 G; 2553 T; 0 other;  
Query Match 7.8%; Score 89; DB 21; Length 11674;  
Best Local Similarity 100.0%; Pred. No. 5.1e-33;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 422 GGAAGCATAGGAGGTTTGAATGGACCGGGAACCTAAGAGTGCCAGATCTGTGCTGAG 481  
DB 4109 GGAAGCATAGGAGGTTTGAATGGACCGGGAACCTAAGAGTGCCAGATCTGTGCTGAG 4168  
QY 482 TGTAAATAGGCTGCATCTCTGTGAGGAAGG 510  
DB 4169 TGTAAATAGGCTGCATCTCTGTGAGGAAGG 4197  
RESULT 15  
AAC86936  
ID AAC86936 standard; DNA; 12119 BP.  
XX  
AC AAC86936;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of a chimeric BVDV/HCV virus.  
XX  
KW Chimeric virus; bovine viral diarrhoea virus; BVDV; hepatitis C virus;  
KW HCV; vaccine; viral inhibitor; antiviral; ss.  
XX  
OS Synthetic.  
OS Bovine viral diarrhoea virus.  
OS Hepatitis C virus.  
XX  
PH Key Location/Qualifiers  
FT CDS 386..11893  
FT /\*tag= a  
XX  
PN WO200075352-A2.  
XX  
PD 14-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-US15527.  
XX  
PR 04-JUN-1999; 99US-0137817.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Nam J, Bukh J, Emerson SU, Purcell RH;  
XX  
XX WPI; 2001-071081/08.  
DR P-PSDB; AAB31167.  
XX  
PT New nucleic acid comprising a chimeric bovine viral diarrhoea virus  
PT genome in which the (non-)structural region has been replaced by  
PT hepatitis C virus (HCV) genome useful for treating or preventing HCV  
PT signs and symptoms -  
XX  
PS Disclosure; Page 62-66; 97pp; English.  
XX

CC The specification describes a nucleic acid comprising a chimeric virus  
CC genome, specifically bovine viral diarrhoea virus (BVDV) genome in which  
CC the (non-)structural region has been replaced by the (non-)structural  
CC region of a hepatitis C virus (HCV) genome. The nucleic acids comprising  
CC the chimeric virus and the chimeric virus are useful for identifying  
CC cell lines capable of supporting the replication of these chimeric  
CC viruses, in screening for neutralizing antibodies to HCV of different  
CC genotypes, in the production of HCV-BVDV virions, for the development  
CC of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal,  
CC in studying the molecular properties of HCV indirectly in vitro, and in  
CC identifying inhibitors of viral enzyme activity which would be useful  
CC as antiviral agents. Formulations or compositions comprising the  
CC chimeric virions may be used to treat or prevent the signs and symptoms  
CC of HCV. The present sequence represents a chimeric nucleic acid of the  
CC invention.

XX  
SQ Sequence 12119 BP; 3589 A; 2668 C; 3211 G; 2651 T; 0 other;  
Query Match 7.8%; Score 89; DB 22; Length 12119;  
Best Local Similarity 100.0%; Pred. No. 5.1e-33;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 422 GGAAAGCATAGAGGTTTGAATGGACCGGGAACCTAAGAGTGCCAGATACTGTGCTGAG 481  
Db 4553 GGAAAGCATAGAGGTTTGAATGGACCGGGAACCTAAGAGTGCCAGATACTGTGCTGAG 4612  
Qy 482 TGTAAATAGGCTGCATCCTCTGAGGAGG 510  
Db 4613 TGTAAATAGGCTGCATCCTCTGAGGAGG 4641

Search completed: December 22, 2003, 18:00:44  
Job time : 360 secs

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OM nucleic - nucleic search, using sw model

Run on: December 22, 2003, 19:13:25 ; Search time 405 Seconds  
(without alignments)  
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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

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- 5: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq.\*
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- 7: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/prodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/prodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1147	100.0	2343	13	US-10-094-749-657
2	1142	99.6	3090	13	Sequence 657, App
3	1047	91.3	2945	15	Sequence 19835, A
4	634	55.3	754	13	Sequence 12415, A
5	634	55.3	754	15	US-10-096-534-43
6	453	39.5	7453	11	US-10-097-340-182
7	276	24.1	443	13	US-09-764-891-8949
8	257	22.4	259	13	Sequence 8949, App
9	257	22.4	259	13	Sequence 14171, A
10	204	17.8	2066	13	US-09-814-353-1471
11	130	11.3	339	10	US-09-814-353-1424
12	89	7.8	12572	15	Sequence 7786, App
13	89	7.8	14078	15	Sequence 1448, App
14	89	7.8	16713	15	Sequence 8500, App
15	80	7.0	510	13	Sequence 10, Appl
					Sequence 1, Appl
					Sequence 9, Appl
					Sequence 4106, App

C 16	80	7.0	510	13	US-09-814-353-10412	Sequence 10412, A
C 17	80	7.0	598	13	US-09-814-353-16796	Sequence 16796, A
C 18	75	6.5	621	15	US-10-198-846-3074	Sequence 3074, App
C 19	48	4.2	663	13	US-10-027-632-221177	Sequence 221177, A
C 20	48	4.2	663	13	US-10-027-632-221178	Sequence 221178, A
C 21	48	4.2	663	14	US-10-027-632-221177	Sequence 221177, A
C 22	48	4.2	663	14	US-10-027-632-221178	Sequence 221178, A
C 23	44	3.8	72604	13	US-10-162-497-7	Sequence 7, Appl
C 24	43	3.7	108317	13	US-10-017-161-2143	Sequence 2143, App
C 25	42	3.7	836	13	US-10-027-632-119193	Sequence 119193, A
C 26	42	3.7	836	14	US-10-027-632-119193	Sequence 119193, A
C 27	42	3.7	5862	11	US-09-764-891-7363	Sequence 7363, App
C 28	42	3.7	28001	14	US-10-193-295-3	Sequence 3, Appl
C 29	42	3.7	32249	11	US-09-764-891-7364	Sequence 7364, App
C 30	40	3.5	1116	11	US-09-822-846-514	Sequence 514, App
C 31	39	3.4	267	15	US-10-060-036-3725	Sequence 59, Appl
C 32	39	3.4	431	10	US-09-962-832-59	Sequence 7581, App
C 33	39	3.4	650	15	US-10-198-846-7581	Sequence 171114, A
C 34	39	3.4	760	13	US-10-027-632-171114	Sequence 171114, A
C 35	39	3.4	760	14	US-10-027-632-171114	Sequence 259505, A
C 36	39	3.4	907	13	US-10-027-632-259505	Sequence 259505, A
C 37	39	3.4	907	14	US-10-027-632-259505	Sequence 261923, A
C 38	39	3.4	1132	13	US-10-027-632-261923	Sequence 261923, A
C 39	39	3.4	1132	14	US-10-027-632-261923	Sequence 261923, A
C 40	38	3.3	2913	13	US-10-027-632-112023	Sequence 112023, A
C 41	38	3.3	2913	13	US-10-027-632-112024	Sequence 112024, A
C 42	38	3.3	2913	14	US-10-027-632-112023	Sequence 112023, A
C 43	38	3.3	2913	14	US-10-027-632-112024	Sequence 112024, A
C 44	38	3.3	6320	9	US-09-764-878-360	Sequence 360, App
C 45	38	3.3	6320	15	US-10-079-854-360	Sequence 360, App

#### ALIGNMENTS

#### RESULT 1

US-10-094-749-657  
; Sequence 657, Application US/10094749  
; Publication No. US20030219741A1  
; GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: OTSUKI, TETSUJI  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: SATO, HIROYUKI  
; APPLICANT: ISHII, SHIZUKO  
; APPLICANT: YAMAMOTO, JUN-ICHI  
; APPLICANT: ISONO, YUUKO  
; APPLICANT: HIO, YURI  
; APPLICANT: OTSUKA, KAORU  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: IRIE, RYOTARO  
; APPLICANT: TAMECHIKA, ICHIRO  
; APPLICANT: SEKI, NAOHICO  
; APPLICANT: YOSHIKAWA, TSUTOMU  
; APPLICANT: OTSUKA, MOTOYUKI  
; APPLICANT: NAGAHARI, KENJI  
; APPLICANT: MASUHO, YASUHIKO  
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA  
; FILE REFERENCE: 084335/0160  
; CURRENT APPLICATION NUMBER: US/10/094,749  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/350,435  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: JP 2001-328381  
; NUMBER OF SEQ ID NOS: 3381  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 657  
; LENGTH: 2343  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-094-749-657

Query Match									
Best Local Similarity 100.0%; Score 1147; DB 13; Length 2343;									
Matches 1147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GCCTTGGGTCAAGCAGAAATATTAATAGGACGGGAATGCACTGTAGCTAGTGGCGCTA	60						
DB	445	GCCTTGGGTCAAGCAGAAATATTAATAGGACGGGAATGCACTGTAGCTAGTGGCGCTA	504						
QY	61	CTGCCAGCCTGAAGAGGAAGTGGCTCGACTCTTGACCATGGCTGGGTTCTTGAGGATGA	120						
DB	505	CTGCCAGCCTGAAGAGGAAGTGGCTCGACTCTTGACCATGGCTGGGTTCTTGAGGATGA	564						
QY	121	GCTAAACCTTTCCATGTACTGGGGTTGAGGCCACAGCATCAGATGTTGAACCTGAAGAA	180						
DB	565	GCTAAACCTTTCCATGTACTGGGGTTGAGGCCACAGCATCAGATGTTGAACCTGAAGAA	624						
QY	181	GGCCTATAGACAGCTGGCAGTGTGTTTCATCTGACAAAAATCATCATCCCGGGCTGA	240						
DB	625	GGCCTATAGACAGCTGGCAGTGTGTTTCATCTGACAAAAATCATCATCCCGGGCTGA	684						
QY	241	GGAGGCTTCAAGGTTTTCGGAGCAGCTTGGGACATTTGACGAATGCTGAAAAACGGAAA	300						
DB	685	GGAGGCTTCAAGGTTTTCGGAGCAGCTTGGGACATTTGACGAATGCTGAAAAACGGAAA	744						
QY	301	GGAGTATGATCAACAGATGCGACAGAAATGAGCTGAGCCGGTCAGTAAATGAGTTTCT	360						
DB	745	GGAGTATGATCAACAGATGCGACAGAAATGAGCTGAGCCGGTCAGTAAATGAGTTTCT	804						
QY	361	GTCCAAAGCTGCAAGATGACTCAAGAGGCAATGAATACTATGATGTGAGCCGATGCCA	420						
DB	805	GTCCAAAGCTGCAAGATGACTCAAGAGGCAATGAATACTATGATGTGAGCCGATGCCA	864						
QY	421	AGGAAAGCATAGAGGTTTGAATGGACCGGGAACCTAAGATGCGCAGATCTGTGCTGA	480						
DB	865	AGGAAAGCATAGAGGTTTGAATGGACCGGGAACCTAAGATGCGCAGATCTGTGCTGA	924						
QY	481	GTGTAATAGCTGCATCTCTGAGAAAGGAGACTTTTGGGAGAGTCAAGCATGTTGGG	540						
DB	925	GTGTAATAGCTGCATCTCTGAGAAAGGAGACTTTTGGGAGAGTCAAGCATGTTGGG	984						
QY	541	CCTCAAGATCACTACTTTGCACTGATGATGAAGGTGTATGACATCACAGAGTGGGC	600						
DB	985	CCTCAAGATCACTACTTTGCACTGATGATGAAGGTGTATGACATCACAGAGTGGGC	1044						
QY	601	TGGATGCCAGCGTGTAGGTATCTCCCGAGATACCCACAGAGTCCCTTATCATCTCATTT	660						
DB	1045	TGGATGCCAGCGTGTAGGTATCTCCCGAGATACCCACAGAGTCCCTTATCATCTCATTT	1104						
QY	661	TGTTTCTCGAATCCAGGACCCAGAGGGCGGAGAGACCCACAGATGCCCTCCTGC	720						
DB	1105	TGTTTCTCGAATCCAGGACCCAGAGGGCGGAGAGACCCACAGATGCCCTCCTGC	1164						
QY	721	TGATCTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCCCGAGGAGATGCCCAATGG	780						
DB	1165	TGATCTCAGGATTTCTTGAGTCGGATCTTTCAAGTACCCCGAGGAGATGCCCAATGG	1224						
QY	781	GAACTTCTTTGAGCTCTCTCAGCTCGCCCTGGAGCGCTGACGCTCTTAAGCCCAACAG	840						
DB	1225	GAACTTCTTTGAGCTCTCTCAGCTCGCCCTGGAGCGCTGACGCTCTTAAGCCCAACAG	1284						
QY	841	CACAGTACCCAGGGAGAGCCAAACCTTAAGCGGCGGAAGAAAGTGAGGAGGCCCTTCCA	900						
DB	1285	CACAGTACCCAGGGAGAGCCAAACCTTAAGCGGCGGAAGAAAGTGAGGAGGCCCTTCCA	1344						
QY	901	ACGTTGATGCCCTTCTTTTCTCAATCAATGTGAGGAGTCAAAAGGGCTGTAGCAC	960						
DB	1345	ACGTTGATGCCCTTCTTTTCTCAATCAATGTGAGGAGTCAAAAGGGCTGTAGCAC	1404						
QY	961	AGGATGAGGTTGATTTATCCCTCCCTCCCAACACCTAGGAACTGAATCTTTTCTTTT	1020						
DB	1405	AGGATGAGGTTGATTTATCCCTCCCTCCCAACACCTAGGAACTGAATCTTTTCTTTT	1464						

QY	1021	TATTTTTGAGATGGAGTCTTGCTCTGTGTCCCGAGCTGGAGTGAGTGTGATCTCAG	1080						
DB	1465	TATTTTTGAGATGGAGTCTTGCTCTGTGTCCCGAGCTGGAGTGAGTGTGATCTCAG	1524						
QY	1081	CTTACTGCAACCTCTGTCTCCCGGTTCAAGCAATCTCCCATCTCAGCCTCCTGAGTAG	1140						
DB	1525	CTTACTGCAACCTCTGTCTCCCGGTTCAAGCAATCTCCCATCTCAGCCTCCTGAGTAG	1584						
QY	1141	CTGGGAT 1147							
DB	1585	CTGGGAT 1591							
RESULT 2									
US-09-814-353-19835/C									
; Sequence 19835, Application US/09814353									
; Publication No. US20030165831A1									
; GENERAL INFORMATION:									
; APPLICANT: Thompson, Pamela									
; APPLICANT: Lillie, James									
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR									
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND									
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER									
; FILE REFERENCE: MRI-006B									
; CURRENT APPLICATION NUMBER: US/09/814,353									
; CURRENT FILING DATE: 2001-03-21									
; PRIOR APPLICATION NUMBER: US 60/191,031									
; PRIOR FILING DATE: 2000-03-21									
; PRIOR APPLICATION NUMBER: US 60/207,124									
; PRIOR FILING DATE: 2000-05-25									
; PRIOR APPLICATION NUMBER: US 60/211,940									
; PRIOR FILING DATE: 2000-06-15									
; PRIOR APPLICATION NUMBER: US 60/216,820									
; PRIOR FILING DATE: 2000-07-07									
; PRIOR APPLICATION NUMBER: US 60/220,661									
; PRIOR FILING DATE: 2000-07-25									
; PRIOR APPLICATION NUMBER: US 60/257,672									
; PRIOR FILING DATE: 2000-12-21									
; NUMBER OF SEQ ID NOS: 22037									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 19835									
; LENGTH: 3090									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; FEATURE:									
; NAME/KEY: misc feature									
; LOCATION: 488..525									
; OTHER INFORMATION: n = A,T,C or G									
US-09-814-353-19835									
Query Match 99.6%; Score 1142; DB 13; Length 3090;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GCCTTGGGTCAAGCAGAAATATTAATAGGACGGGAATGCACCTGTAGCTAGTGGCGCTA	60						
DB	1667	GCCTTGGGTCAAGCAGAAATATTAATAGGACGGGAATGCACCTGTAGCTAGTGGCGCTA	1608						
QY	61	CTGCCAGCCTGAAGAGGAAGTGGCTCGACTTTGACCATGGCTGGGTTCTTGAGGATGA	120						
DB	1607	CTGCCAGCCTGAAGAGGAAGTGGCTCGACTTTGACCATGGCTGGGTTCTTGAGGATGA	1548						
QY	121	GCTAAACCTTTTCCATGTACTGCGGGTTGAGGCCACAGCATCAGATGTTGAACCTGAAGAA	180						
DB	1547	GCTAAACCTTTTCCATGTACTGCGGGTTGAGGCCACAGCATCAGATGTTGAACCTGAAGAA	1488						
QY	181	GGCCTATAGACAGCTGGCAGTGTGTTTCATCTGACAAAAATCATCATCCCGGGCTGA	240						
DB	1487	GGCCTATAGACAGCTGGCAGTGTGTTTCATCTGACAAAAATCATCATCCCGGGCTGA	1428						
QY	241	GGAGGCTTCAAGGTTTTCGGAGCAGCTTGGGACATTTGAGCAATGCTGAAAAACGGAAA	300						





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RESULT 6
US-09-764-891-8949
; Sequence 8949, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8949
; LENGTH: 7453

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RESULT 7
US-09-814-353-14171/c
; Sequence 14171, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0

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US-09-814-353-14171/C

; Sequence 14171, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Thompson, Pamela

; APPLICANT: Lillie, James

; TITLE OF INVENTION: NOVEL

; TITLE OF INVENTION: IDENT

; TITLE OF INVENTION: THERA

; FILE REFERENCE: MRI-006B

; CURRENT APPLICATION NUMBER

; CURRENT FILING DATE: 2001

;  
PRIOR APPLICATION NUMBER:

; PRIOR FILING DATE: 2000-03-

;  
PRIOR APPLICATION NUMBER:

; PRIOR FILING DATE: 2000-09-

10 ; PRIOR APPLICATION NUMBER: 10

; PRIOR FILING DATE: 2000-06-01

; PRIOR APPLICATION NUMBER:  
 ; PRIOR FILING DATE: 2000 03

; PRIOR FILING DATE: 2000-07-  
; PRIOR APPLICATION NUMBER:

;; PRIOR APPLICATION NUMBER:  
: PRIOR FILING DATE: 2000 03

;; PRIOR FILING DATE: 2000-07-11  
: PRIOR APPLICATION NUMBER:

: PRIOR FILING DATE: 3000 13  
 : PRIOR APPLICATION NUMBER:

; PRIOR FILING DATE: 2000-12-  
 ; NUMBER OF SEQ IN NOS: 3303

NUMBER OF SEQ ID NOS: 2203  
SOFTWARE: FastSeq for Windows

SOFTWARE: FASTSEQ FOR WIND

Qy 184 CTATAGACAGCTGGCAGTGATGTTTCATCTCGACAAAAATCATCATCCCCGGGCTGAGGA 243  
Db 259 CTATAGACAGCTGGCAGTGATGTTTCATCTCGACAAAAATCATCATCCCCGGGCTGAGGA 200  
Qy 244 GGCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCAATGCTGAGAAAGCGAAAGGA 303  
Db 199 GGCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCAATGCTGAGAAAGCGAAAGGA 140  
Qy 304 GTATGAGATGAAGCAAGATGCGACAGAGATGAGCTGAGCCGTCAGTAAATGAGTTTCTGTC 363  
Db 139 GTATGAGATGAAGCAAGATGCGACAGAGATGAGCTGAGCCGTCAGTAAATGAGTTTCTGTC 80  
Qy 364 CAAGCTCAAGATGACCTCAAGGAGGCAATGAATATCTATGATGTGTAGCCGATGCCAAGG 423  
Db 79 CAAGCTCAAGATGACCTCAAGGAGGCAATGAATATCTATGATGTGTAGCCGATGCCAAGG 20  
Qy 424 AAAGCATAGGAGGTTTG 440  
Db 19 AAAGCATAGGAGGTTTG 3

RESULT 9  
US-09-814-353-7786/c  
; Sequence 7786, Application US/09814353  
; Publication No. US20030165831A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Pamela  
; APPLICANT: Lee, John  
; APPLICANT: Lillie, James  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER  
; FILE REFERENCE: MRI-006B  
; CURRENT APPLICATION NUMBER: US/09/814,353  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,031  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/207,124  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: US 60/211,940  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: US 60/216,820  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/220,661  
; PRIOR FILING DATE: 2000-07-25  
; PRIOR APPLICATION NUMBER: US 60/257,672  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 22037  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7786  
; LENGTH: 259  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1, 2\_  
; OTHER INFORMATION: n = A,T,C or G  
US-09-814-353-7786

Query Match 22.4%; Score 257; DB 13; Length 259;  
Best Local Similarity 100.0%; Pred. No. 2.5e-130;  
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 CTATAGACAGCTGGCAGTGATGTTTCATCTCGACAAAAATCATCATCCCCGGGCTGAGGA 243  
Db 259 CTATAGACAGCTGGCAGTGATGTTTCATCTCGACAAAAATCATCATCCCCGGGCTGAGGA 200  
Qy 244 GGCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCAATGCTGAGAAAGCGAAAGGA 303  
Db 199 GGCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCAATGCTGAGAAAGCGAAAGGA 140  
Qy 304 GTATGAGATGAAGCAAGATGCGACAGAGATGAGCTGAGCCGTCAGTAAATGAGTTTCTGTC 363

Qy 166 TGTGAAGTGAAGAGGGCTATAGACAGCTGGCAGTGATGTTTCATCTCGACAAAAATCA 225  
Db 392 TGTGAAGTGAAGAGGGCTATAGACAGCTGGCAGTGATGTTTCATCTCGACAAAAATCA 333  
Qy 226 TCATCCCCGGGCTGAGGAGCCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCAA 285  
Db 332 TCATCCCCGGGCTGAGGAGCCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCAA 273  
Qy 286 TGCTGAAAGCCAAAGGAGTATGAGATGAACGAATGCGACAGATGAGCTGAGCCGTC 345  
Db 272 TGCTGAAAGCCAAAGGAGTATGAGATGAACGAATGCGACAGATGAGCTGAGCCGTC 213  
Qy 346 AGTAATGAGTTTCTGTCAGAGCTCAAGATGACCTCAAGGAGGCAATGAATATCTATGAT 405  
Db 212 AGTAATGAGTTTCTGTCAGAGCTCAAGATGACCTCAAGGAGGCAATGAATATCTATGAT 153  
Qy 406 GTGTAGCCGATGCCAAGGAAAGCATAGGAGGTTTGA 441  
Db 152 GTGTAGCCGATGCCAAGGAAAGCATAGGAGGTTTGA 117

RESULT 8  
US-09-814-353-1424/c  
; Sequence 1424, Application US/09814353  
; Publication No. US20030165831A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Pamela  
; APPLICANT: Lee, John  
; APPLICANT: Lillie, James  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER  
; FILE REFERENCE: MRI-006B  
; CURRENT APPLICATION NUMBER: US/09/814,353  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,031  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/207,124  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: US 60/211,940  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: US 60/216,820  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/220,661  
; PRIOR FILING DATE: 2000-07-25  
; PRIOR APPLICATION NUMBER: US 60/257,672  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 22037  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1424  
; LENGTH: 259  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1, 2\_  
; OTHER INFORMATION: n = A,T,C or G  
US-09-814-353-1424

Query Match 22.4%; Score 257; DB 13; Length 259;  
Best Local Similarity 100.0%; Pred. No. 2.5e-130;  
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 TGTGAAGTGAAGAGGGCTATAGACAGCTGGCAGTGATGTTTCATCTCGACAAAAATCA 225  
Db 392 TGTGAAGTGAAGAGGGCTATAGACAGCTGGCAGTGATGTTTCATCTCGACAAAAATCA 333  
Qy 226 TCATCCCCGGGCTGAGGAGCCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCAA 285  
Db 332 TCATCCCCGGGCTGAGGAGCCCTTCAAGGTTTTTGGAGCAGCTTTGGGACATTGTGAGCAA 273  
Qy 286 TGCTGAAAGCCAAAGGAGTATGAGATGAACGAATGCGACAGATGAGCTGAGCCGTC 345  
Db 272 TGCTGAAAGCCAAAGGAGTATGAGATGAACGAATGCGACAGATGAGCTGAGCCGTC 213  
Qy 346 AGTAATGAGTTTCTGTCAGAGCTCAAGATGACCTCAAGGAGGCAATGAATATCTATGAT 405  
Db 212 AGTAATGAGTTTCTGTCAGAGCTCAAGATGACCTCAAGGAGGCAATGAATATCTATGAT 153  
Qy 406 GTGTAGCCGATGCCAAGGAAAGCATAGGAGGTTTGA 441  
Db 152 GTGTAGCCGATGCCAAGGAAAGCATAGGAGGTTTGA 117

Db 139 GTATGAGATGAAACGAATGCGAGAGATGAGCTGAGCCGGTCAGTAAATGAGTTTCTGTC 80
QY 364 CAAGCTGCAGATGACCTCAAGGAGGCAATGATATCATGTGTAGCGGATGCCAAGG 423
Db 79 CAAGCTGCAGATGACCTCAAGGAGGCAATGATATCATGTGTAGCGGATGCCAAGG 20
QY 424 AAAGCATAGGAGTTTG 440
Db 19 AAAGCATAGGAGTTTG 3
RESULT 10
US-10-094-749-1448
; Sequence 1448, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISENO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKI, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1448
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-1448
Query Match 17.8%; Score 204; DB 13; Length 2066;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 944 CAAAAGGGCTGTAGCAGAGTGGAGTTTGATTTATCCCTCTCCGCCCAACACCTAGGAA 1003
Db 1104 CAAAAGGGCTGTAGCAGAGTGGAGTTTGATTTATCCCTCTCTCCGCCCAACACCTAGGAA 1163
QY 1004 CTGAATCTTTTCTTTTATTTTGGAGTGGAGTCTGCTCTGTTGCCAGCTGGAGTG 1063
Db 1164 CTGAATCTTTTCTTTTATTTTGGAGTGGAGTCTGCTCTGTTGCCAGCTGGAGTG 1223
QY 1064 CAGTGTGTGATCTCAGCTTACTGCAACCTCTGCTCCGGGTTCAAGCAATCTCCCAT 1123
Db 1224 CAGTGTGTGATCTCAGCTTACTGCAACCTCTGCTCCGGGTTCAAGCAATCTCCCAT 1283
QY 1124 CTCAGCCTCTCAGTAGCTGGGAT 1147
Db 1284 CTCAGCCTCTCAGTAGCTGGGAT 1307

RESULT 11
US-09-867-701-8500

; Sequence 8500, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8500
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8500
Query Match 11.3%; Score 130; DB 10; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.6e-60;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 899 CAACGTTGATGCCCTTCTCTTCTCAATCAATGTCTCAGGAGTCAAAAGGGCTGTAGC 958
Db 26 CAACGTTGATGCCCTTCTCTTCTCAATCAATGTCTCAGGAGTCAAAAGGGCTGTAGC 85
QY 959 ACAGGATGGAGTTTGATTTATCCCTCTCCGCCCAACACCTAGGACTGAATCTTTTCTT 1018
Db 86 ACAGGATGGAGTTTGATTTATCCCTCTCCGCCCAACACCTAGGAACTGAATCTTTTCTT 145
QY 1019 TTTATTTT 1028
Db 146 TTTATTTT 155
RESULT 12
US-10-228-406A-10
; Sequence 10, Application US/10228406A
; Publication No. US20030104612A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Xuemei
; APPLICANT: Zybaurth, Gabriele
; TITLE OF INVENTION: GENERATION OF TYPE I/TYPE II HYBRID FORM OF BOVINE
; TITLE OF INVENTION: VIRAL DIARRHEA VIRUS FOR USE AS VACCINE
; FILE REFERENCE: PC11051A
; CURRENT APPLICATION NUMBER: US/10/228,406A
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 12572
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid BVD virus NADL890
US-10-228-406A-10
Query Match 7.8%; Score 89; DB 15; Length 12572;
Best Local Similarity 79.8%; Pred. No. 6.5e-38;
Matches 71; Conservative 18; Mismatches 0; Indels 0; Gaps 0;
QY 422 GGAAGCATAGGAGTTTGAATGGACCGGAACTAAGAGTGCCAGATCTGTGCTGAG 481
Db 5006 GGAAGCAUAGAGAGGUUGAANUGACCGGAACTAAGAGTGCCAGUACUGUGCUGAG 5065
QY 482 TGTAAATAGGTCATCTCTGTGAGGAAGG 510
Db 5066 UGUAAUAGGCGUCAUCCUGCUGAGGAAGG 5094

RESULT 13
US-10-134-288-1

Sequence 1, Application US/10134288  
Publication No. US20030165520A1  
GENERAL INFORMATION:  
APPLICANT: Lee, John  
APPLICANT: Thompson, Pamela  
APPLICANT: Lillie, James  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
THERAPY OF OVARIAN CANCER  
FILE REFERENCE: MRI-006B  
CURRENT APPLICATION NUMBER: US/09/814,353  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: US 60/191,031  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/207,124  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 60/211,940  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: US 60/216,820  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: US 60/220,661  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/257,672  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 22037  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4106  
LENGTH: 510  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 32  
OTHER INFORMATION: n = A,T,C or G  
US-09-814-353-4106

Query Match 7.0%; Score 80; DB 13; Length 510;  
Best Local Similarity 99.2%; Pred. No. 5e-33; Indels 0; Gaps 0;  
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCTTGGGTCACGACGAATATTATAGGCGAGGGAATGCACCTGTAGCTAGTGGGCGCTA 60  
Db 163 GCCTTGGGTCACGACGAATATTATAGGCGAGGGAATGCACCTGTAGCTAGTGGGCGCTA 104

Qy 61 CTGCCAGCCTGGAAGAGGAGTGGCTCGACTCTTTGACCATGGCTGCGGTTCTCTGAGGATGA 120  
Db 103 CTGCCAGCCTGGAAGAGGAGTGGCTCGACTCTTTGACCATGGCTGCGGTTCTCTGAGGATGA 44

Qy 121 GCTAAACCCCTT 131  
Db 43 GCTAAACCCCTT 33

Search completed: December 22, 2003, 21:21:26  
Job time : 407 secs

Sequence 1, Application US/10134288  
Publication No. US20030165520A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Xuemei  
APPLICANT: Sheppard, Mike  
TITLE OF INVENTION: ATTENUATED FORMS OF BOVINE VIRAL DIARRHEA VIRUS  
FILE REFERENCE: PC10435A  
CURRENT APPLICATION NUMBER: US/10/134,288  
CURRENT FILING DATE: 2002-04-29  
PRIOR APPLICATION NUMBER: US/09/702,330  
PRIOR FILING DATE: 2000-10-31  
PRIOR APPLICATION NUMBER: 09/433,262  
PRIOR FILING DATE: 1999-11-04  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 14078  
TYPE: DNA  
ORGANISM: Bovine Viral Diarrhea Virus  
US-10-134-288-1

Query Match 7.8%; Score 89; DB 13; Length 14078;  
Best Local Similarity 100.0%; Pred. No. 6.5e-38; Indels 0; Gaps 0;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 422 GGAAGCATAGGAGTTTGAATGACCGGAACTTAAGTGCCAGATACTGTGCTGAG 481  
Db 4550 GGAAGCATAGGAGTTTGAATGACCGGAACTTAAGTGCCAGATACTGTGCTGAG 4609

Qy 482 TGTATAGGCTGCATCTCTGCTGAGGAGG 510  
Db 4610 TGTATAGGCTGCATCTCTGCTGAGGAGG 4638

RESULT 14  
US-10-228-406A-9  
Sequence 9, Application US/10228406A  
Publication No. US20030104612A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Xuemei  
APPLICANT: Zybarrh, Gabriele  
TITLE OF INVENTION: GENERATION OF TYPE I/TYPE II HYBRID FORM OF BOVINE  
VIRAL DIARRHEA VIRUS FOR USE AS VACCINE  
FILE REFERENCE: PC11051A  
CURRENT APPLICATION NUMBER: US/10/228,406A  
CURRENT FILING DATE: 2002-08-27  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 16713  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: pNADL890 vector  
US-10-228-406A-9

Query Match 7.8%; Score 89; DB 15; Length 16713;  
Best Local Similarity 100.0%; Pred. No. 6.6e-38; Indels 0; Gaps 0;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 422 GGAAGCATAGGAGTTTGAATGACCGGAACTTAAGTGCCAGATACTGTGCTGAG 481  
Db 5006 GGAAGCATAGGAGTTTGAATGACCGGAACTTAAGTGCCAGATACTGTGCTGAG 5085

Qy 482 TGTATAGGCTGCATCTCTGCTGAGGAGG 510  
Db 5066 TGTATAGGCTGCATCTCTGCTGAGGAGG 5094

RESULT 15  
US-09-814-353-4106/c  
Sequence 4106, Application US/09814353  
Publication No. US20030165831A1

OM nucleic - nucleic search, using sw model  
Run on: December 22, 2003, 17:14.33 : Search time 2750. Seconds  
(without alignments)  
10137.176 Million cell updates/sec

Title: US-10-049-742-22  
Perfect score: 1147  
Sequence: 1 gctctgggtcaacagagaata.....gcctctctgagtagctgggat 1147

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0  
Searched: 22781392 seqs, 12152238056 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
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7: em\_esthum:\*  
8: em\_esthum:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estfun:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_hum:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_fun:\*  
24: em\_gss\_fun:\*  
25: em\_gss\_fun:\*  
26: em\_gss\_fun:\*  
27: em\_gss\_fun:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	704	61.4	918	13	BU956189
2	692	60.3	957	12	BM802135
3	663	57.8	942	13	BU538214
4	639	55.7	906	10	BM676002

5	635	55.4	878	12	BG763500
6	635	55.4	995	12	BM452174
7	622	54.2	1046	12	BM802913
8	607	52.9	904	13	BQ691177
9	605	52.7	605	13	BX090711
10	585	51.0	955	13	BU538351
11	565	49.3	1046	12	BQ058270
12	550	48.0	618	12	BM011379
13	542	47.3	723	10	BE779250
14	509	44.4	927	12	BM424147
15	474	41.3	912	10	BG751088
16	441	38.4	723	10	BE519407
17	437	38.1	785	12	B1333110
18	423	36.9	776	12	BG821631
19	417	36.4	469	13	BG504969
20	382	33.3	968	13	B0838931
21	372	32.4	527	12	B1002288
22	366	31.9	874	10	BE679562
23	362	31.6	505	10	BF819630
24	348	30.3	588	9	AA460131
25	317	27.6	741	12	BG761596
26	316	27.6	448	12	B1002295
27	314	27.4	864	10	BQ252385
28	258	22.5	325	14	RI7611
29	257	22.4	621	10	BE385257
30	254	22.1	788	10	BE304441
31	248	21.6	648	13	B0629493
32	226	19.7	338	10	BF902230
33	218	19.0	704	9	AV729617
34	209	18.2	805	10	BE536083
35	207	18.0	596	12	BM823481
36	163	14.2	514	9	AI435045
37	163	14.2	928	10	BG678276
38	146	12.7	859	13	BQ223550
39	145	12.6	940	10	BG328197
40	143	12.5	786	10	BF965963
41	135	11.8	938	12	B1259675
42	130	11.3	339	9	AB908339
43	112	9.8	163	10	BE826354
44	109	9.5	843	13	BQ220945
45	91	7.9	474	13	BQ323294

ALIGNMENTS

BU956189 918 bp mRNA linear EST 21-OCT-2002  
AGENCY: 10613510 NIH\_MGC\_107 Homo sapiens cDNA clone  
IMAGE: 6729715 5', mRNA sequence.  
BU956189  
BU956189.1 GI:24185761  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 918)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM3053 row: f column: 18  
High quality sequence stop: 544.

RESULT 1  
BU956189  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Dec 23 09:41:21 2003

RESULT 2  
BM802135  
LOCUS  
DEFINITIONBM802135  
LOCUS  
DEFINITION

Location/Qualifiers

1. 918

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6729715"

/tissue\_type="adenocarcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/lab\_host="NIH\_MGC\_107"

/clone\_lib="NIH\_MGC\_107"

/note="Organ: breast; Vector: pOTB7; Site\_1: EcoRI;

Site\_2: XhoI; CDNA made by oligo-dt priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGACGAG(G). Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library."

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

234 a 228 c 238 g 218 t

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BM802135

AGENCY: NIH\_MGC\_88 Homo sapiens

5', mRNA sequence.

BM802135.1 GI:19118958

EST.

Homo sapiens (human)

Homo sapiens

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 957)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Ph.D.

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue procurement: ATCC

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1284 row: c column: 24

High quality sequence stop: 621.

Location/Qualifiers

1. 957

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5559503"

/tissue\_type="duodenal adenocarcinoma, cell line"

/lab\_host="NIH\_MGC\_88"

/note="Organ: small intestine; Vector: pCMV-SPORT6;

Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally;

oligo-dt primed. Average insert size 1.767 Kb. Library

enriched for full-length clones and constructed by Life

Technologies. Note: this is a NIH\_MGC Library."

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ORIGIN  
 Query Match 57.8%; Score 663; DB 13; Length 942;  
 Best Local Similarity 99.9%; Pred. No. 2.1e-213;  
 Matches 713; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	182	GCCTATAGACAGCTGGCAGTGATGTTTCATCTCTGACAAAAATCATCATCCCGGGCTGAG	241
Db	1	GCCTATAGACAGCTGGCAGTGATGTTTCATCTCTGACAAAAATCATCATCCCGGGCTGAG	60
Qy	242	GAGGCCTTCAAGGTTTTCGGAGCAGCTTTGGGACATTTGTGAGCAATGCTGAAAAAGCGAAAG	301
Db	61	GAGGCCTTCAAGGTTTTCGGAGCAGCTTTGGGACATTTGTGAGCAATGCTGAAAAAGCGAAAG	120
Qy	302	GAGTATGAGATGAACGAAATGCGACAGAGAAATGAGCTGAGCCGGTCAAGTAATGAGTTTCTG	361
Db	121	GAGTATGAGATGAACGAAATGCGACAGAGAAATGAGCTGAGCCGGTCAAGTAATGAGTTTCTG	180
Qy	362	TCCAGCTGCAAGATGACCTCAAGGAGCGAATGAATACTATGATGTGAGCCGATGCCAA	421
Db	181	TCCAGCTGCAAGATGACCTCAAGGAGCGAATGAATACTATGATGTGAGCCGATGCCAA	240
Qy	422	GGAAAGCATGAGAGGTTTGAATGACCCGGGAACCTTAAGAGTGCCAGATCTGTGCTGAG	481
Db	241	GGAAAGCATGAGAGGTTTGAATGACCCGGGAACCTTAAGAGTGCCAGATCTGTGCTGAG	300
Qy	482	TGTAATAGGCTGCATCTCTGCTGAGGAAGGAGACTTTTGGGCAGAGTCAAGCATCTTGGGC	541
Db	301	TGTAATAGGCTGCATCTCTGCTGAGGAAGGAGACTTTTGGGCAGAGTCAAGCATCTTGGGC	360
Qy	542	CTCAAGATCACTACTTTTGCACTGATGATGGAAGGTGTATGACATCACAGATGGGCT	601
Db	361	CTCAAGATCACTACTTTTGCACTGATGATGGAAGGTGTATGACATCACAGATGGGCT	420
Qy	602	GGATGCCAGCGTGTAGGTATCTCCCAGATACCCACAGAGTCCCCTATCATCTCATTT	661
Db	421	GGATGCCAGCGTGTAGGTATCTCCCAGATACCCACAGAGTCCCCTATCATCTCATTT	480
Qy	662	GGTCTTCGATTCACAGGCACAGAGGGGGCAGAGAGCCACCCAGATGCCCTCCCTGCT	721
Db	481	GGTCTTCGATTCACAGGCACAGAGGGGGCAGAGAGCCACCCAGATGCCCTCCCTGCT	540
Qy	722	GATCTTCAGGATTTCTTGAGTCGATCTTTCAAGTACCCCCAGGGCAGATGCCCAATGGG	781
Db	541	GATCTTCAGGATTTCTTGAGTCGATCTTTCAAGTACCCCCAGGGCAGATGCCCAATGGG	600
Qy	782	AACTTCTTTGAGCTCTCAGCCTGCCCTGGAGCCGCTGCAGCCTCTTAAGCCCAACAGC	841
Db	601	AACTTCTTTGAGCTCTCAGCCTGCCCTGGAGCCGCTGCAGCCTCTTAAGCCCAACAGC	660
Qy	842	ACAGTACCCAGGGAGAACCAACCTTAAGCCGGCGGAAGAAAGTGAGAGGCC	895
Db	661	ACAGTACCCAGGGAGAACCAACCTTAAGCCGGCGGAAGAAAGTGAGAGGCC	714

RESULT 4  
 BG676002  
 LOCUS  
 DEFINITION  
 602622366F1 NCI\_CGAP\_Skn4 Homo sapiens cDNA clone IMAGE:4747337 5',  
 mRNA sequence.  
 BG676002  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 906)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Plate: LLAM12286 row: d column: 07  
High quality sequence start: 5  
High quality sequence stop: 713.

FEATURES

source  
1..1046  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="duodenal adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC 88"  
/note="Organ: small intestine; Vector: pCMV-SPORT6; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."  
224 a 284 c 260 g 276 t 2 others

BASE COUNT

ORIGIN  
224 a 284 c 260 g 276 t 2 others

Query Match

Best Local Similarity 54.12%; Score 622; DB 12; Length 1046;  
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	526	GTCACGATGTTGGGCTCAAGATCACTTGTGCTAGTATCTCCAGATACCCACAGAGTCCC	585
Db	28	GTCACGATGTTGGGCTCAAGATCACTTGTGCTAGTATCTCCAGATACCCACAGAGTCCC	585
Qy	586	CATCACAGATGGGCTGGATGCCAGCGTGTAGTATCTCCAGATACCCACAGAGTCCC	645
Db	88	CATCACAGATGGGCTGGATGCCAGCGTGTAGTATCTCCAGATACCCACAGAGTCCC	645
Qy	646	CTATCACATCTCATTTGGTTCTCGATTCAGGATTCCTGAGTGGATCTTCAAGTACCCCGAG	147
Db	148	CTATCACATCTCATTTGGTTCTCGATTCAGGATTCCTGAGTGGATCTTCAAGTACCCCGAG	147
Qy	706	AGATGCCCTCTGCTGATCTTCAAGTTCCTGAGTGGATCTTCAAGTACCCCGAG	207
Db	208	AGATGCCCTCTGCTGATCTTCAAGTTCCTGAGTGGATCTTCAAGTACCCCGAG	207
Qy	766	GCAGATGCCCAATGGGAATCTTTGAGTGGATCTTCAAGTACCCCGAG	267
Db	268	GCAGATGCCCAATGGGAATCTTTGAGTGGATCTTCAAGTACCCCGAG	267
Qy	826	CTCTAAGCCCAACAGCAGACAGTACCCAGGAGGAGCCAAACCTAAGCGCGGAGGAGT	327
Db	328	CTCTAAGCCCAACAGCAGACAGTACCCAGGAGGAGCCAAACCTAAGCGCGGAGGAGT	327
Qy	886	GAGGAGGCGCTTCCAACTGATGCGCCCTCTCTTCTCTCAAAATCAATGTCAAGGAGTCA	885
Db	388	GAGGAGGCGCTTCCAACTGATGCGCCCTCTCTTCTCTCAAAATCAATGTCAAGGAGTCA	885
Qy	946	AAAGGGCTGTAGCAGAGTGGAGTTTGAATTAATCCCTCTCCCGGTTCAAGCAATCTCCCA	1005
Db	448	AAAGGGCTGTAGCAGAGTGGAGTTTGAATTAATCCCTCTCCCGGTTCAAGCAATCTCCCA	1005
Qy	1006	GAATCTTTTCTTTTATTTTGTAGATGGAGTCTTGTCTGTGTCCTGTCCTGTCCTGTCCT	507
Db	508	GAATCTTTTCTTTTATTTTGTAGATGGAGTCTTGTCTGTGTCCTGTCCTGTCCTGTCCT	507
Qy	1066	GTGGTGTGATCTCAGCTTACTGCAACCTCTGTCTCCCGGTTCAAGCAATCTCTCCCA	1065
Db	568	GTGGTGTGATCTCAGCTTACTGCAACCTCTGTCTCCCGGTTCAAGCAATCTCTCCCA	1065
Qy	1126	CAGCTCTCTGAGTGGGAT 1147	627
Db	628	CAGCTCTCTGAGTGGGAT 649	627

RESULT 8  
Q691177

CCUS

EFINITION BO691177 904 bp mRNA linear EST 15-JUL-2002  
AGENCOURT\_8340957 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6249114

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BO691177  
BO691177.1 GI:21816493  
EST.  
Homo sapiens (human)  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 904)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone Distribution by: Agencourt Bioscience Corporation  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLC2390 row: a column: 19  
High quality sequence stop: 609.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6249114"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
219 a 244 c 239 g 202 t

FEATURES

source  
Location/Qualifiers  
1..904

Query Match

Best Local Similarity 52.9%; Score 607; DB 13; Length 904;  
Matches 607; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	254	GTTCGCGAGCAGTTGGGACATTTGCAGCAATGCTGAAAAGCGAAGGAGTATGAGATG	313
Db	1	GTTCGCGAGCAGTTGGGACATTTGCAGCAATGCTGAAAAGCGAAGGAGTATGAGATG	313
Qy	314	AAACGAATGGCAGAGATGAGTGGCGGTCAGTAAATGAGTTTCTGTCCAGCTGCAA	373
Db	61	AAACGAATGGCAGAGATGAGTGGCGGTCAGTAAATGAGTTTCTGTCCAGCTGCAA	373
Qy	374	GATGACCTCAAGGAGGCAATGAATATCTATGATGTGTAGCCGATCCCAAGAAAGCATAGG	433
Db	121	GATGACCTCAAGGAGGCAATGAATATCTATGATGTGTAGCCGATCCCAAGAAAGCATAGG	433
Qy	434	AGTTTGAATGGACCGGCACTAGAGTCCAGATCTGTCTGAGTGTATAGGCTG	493
Db	181	AGTTTGAATGGACCGGCACTAGAGTCCAGATCTGTCTGAGTGTATAGGCTG	493
Qy	494	CATCTCTGTGAGGAGGAGACTTTGGGCGAGAGTCAAGCATGTTGGGCTCAAGATCACC	553
Db	241	CATCTCTGTGAGGAGGAGACTTTGGGCGAGAGTCAAGCATGTTGGGCTCAAGATCACC	553
Qy	554	TACTTTGCACTGATGGAGGAGTGTATCAGATCAGAGTGGGCTGAGTCCAGCGT	613
Db	301	TACTTTGCACTGATGGAGGAGTGTATCAGATCAGAGTGGGCTGAGTCCAGCGT	613
Qy	614	GTAGGTATCTCCCGAGATCCAGAGTCCCCTATCAGATCTTGGTCTTCGGATT	673

Db 361 GTAGGTATCTCCCCAGATACCCACAGAGTCCCTCATCATCTCATTGGTTCTGGGATT 420  
 QY 674 CCAGGCACAGAGGCGGCAGAGAGCCACCCAGATGCCCTCCTGCTGATCTTCAGGAT 733  
 Db 421 CCAGGCACAGAGGCGGCAGAGAGCCACCCAGATGCCCTCCTGCTGATCTTCAGGAT 480  
 QY 734 TTCTTGAGTGGGATCTTTCAAGTACCCCCAGGCGAGATGCCCAATGGAACTTCTTTGCA 793  
 Db 481 TTCTTGAGTGGGATCTTTCAAGTACCCCCAGGCGAGATGCCCAATGGAACTTCTTTGCA 540  
 QY 794 GTCCTCAGCCCTGCCCTGGAGCGCTGCAGGCCTTAAGCCCAACAGCAGACAGTACCCCAAG 853  
 Db 541 GTCCTCAGCCCTGCCCTGGAGCGCTGCAGGCCTTAAGCCCAACAGCAGACAGTACCCCAAG 600  
 QY 854 GGAGAAAG 860  
 Db 601 GGAGAAAG 607

RESULT 9  
 BX090711  
 LOCUS BX090711 Soares\_total\_fetus\_Nb2HF8 9w Homo sapiens cDNA clone EST 23-JAN-2003  
 DEFINITION IMAGp998P081964 ; IMAGE:796663, mRNA sequence.

ACCESSION BX090711  
 VERSION BX090711.1 GI:27826181

KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 605)  
 Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
 Radelof,U., Schneider,D. and Korn,B.

## AUTHORS

Human Unigeneset - RZPD3

## TITLE

Human Unigeneset - RZPD3

## JOURNAL

Unpublished

## COMMENT

Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGp998P081964.  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/cloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de

This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, Primer sequence: TTTCACACAGAAACAGCTATGAC.

## FEATURES

source

1. 605  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGp998P081964 ; IMAGE:796663"  
 /dev\_stage="8-9 weeks"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares\_total\_fetus\_Nb2HF8\_9w"  
 /note="Vector: p77T3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was prepared from mRNA obtained from pooled 8-9 week  
 (total) fetus material with a Not I - oligo(dT) primer [5'  
 TGTTACCAATCTGAGTGGAGCGCGCTAATTTTTTTTTTTTTTTT 3'].  
 Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified p77T3 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
 ORIGIN

Query Match 52.7%; Score 605; DB 13; Length 605;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-194;  
 Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 466 CAGATACCTGCTGAGTGTAAATAGGCTGCATCTCTGCTGAGAAAGGAGACATTTTGGGCAGA 525  
 Db 1 CAGATACCTGCTGAGTGTAAATAGGCTGCATCTCTGCTGAGAAAGGAGACATTTTGGGCAGA 60  
 QY 526 GTCAGACATGTTGGGCTCAAGATCACCTACTTTGCACTGATGATGGAAGGTGTATGA 585  
 Db 61 GTCAGACATGTTGGGCTCAAGATCACCTACTTTGCACTGATGATGGAAGGTGTATGA 120  
 QY 586 CATCACAGAGTGGGCTGGATGCCAGCGGTAGGTATCTCCCCAGATACCCACAGAGTCCCC 645  
 Db 121 CATCACAGAGTGGGCTGGATGCCAGCGGTAGGTATCTCCCCAGATACCCACAGAGTCCCC 180  
 QY 646 CTATCACATCTCAATTTGGTTCTCGGATTCAGAGCGCGGAGAGACGACACCCC 705  
 Db 181 CTATCACATCTCAATTTGGTTCTCGGATTCAGAGCGCGGAGAGACGACACCCC 240  
 QY 706 AGATGCCCCCTCCTGCTGATCTTCAGGATTTCTTGAATCGGATCTTTCAAGTACCCCGAGG 765  
 Db 241 AGATGCCCCCTCCTGCTGATCTTCAGGATTTCTTGAATCGGATCTTTCAAGTACCCCGAGG 300  
 QY 766 GCAGATGCCCAATGGGAACTTCTTTGAGCTCTCTAGCTGCCCTGGAGCGCGCTGAGC 825  
 Db 301 GCAGATGCCCAATGGGAACTTCTTTGAGCTCTCTAGCTGCCCTGGAGCGCGCTGAGC 360  
 QY 826 CTCTAAGCCCAACAGACACAGTACCCAGGAGAGCAACCTTAAGCGCGGAGAGAAAGT 885  
 Db 361 CTCTAAGCCCAACAGACACAGTACCCAGGAGAGCAACCTTAAGCGCGGAGAGAAAGT 420  
 QY 886 GAGGAGGCCCTTCCAACTGATGCCCTTCTTTCTTCAATCAATGTCAAGGAGTCA 945  
 Db 421 GAGGAGGCCCTTCCAACTGATGCCCTTCTTTCTTCAATCAATGTCAAGGAGTCA 480  
 QY 946 AAGAGGCTGAGACAGGATGGAGTTGATTTATCCCTCTCCCTCCCAACACCTAGGAAC 1005  
 Db 481 AAGAGGCTGAGACAGGATGGAGTTGATTTATCCCTCTCCCTCCCAACACCTAGGAAC 540  
 QY 1006 GAATCTTTTCTTTTATTTTGTAGATGAGTCTTGTCTGTTCCTGCTGAGTGA 1065  
 Db 541 GAATCTTTTCTTTTATTTTGTAGATGAGTCTTGTCTGTTCCTGCTGAGTGA 600  
 QY 1066 GTGGT 1070  
 Db 601 GTGGT 605

RESULT 10

BUS38351

LOCUS

DEFINITION

AGENCOURT\_10181238 NIH\_MGC\_107 Homo sapiens cDNA clone

IMAGE:6568891 5', mRNA sequence.

ACCESSION

BUS38351

VERSION

BUS38351.1 GI:22848792

KEYWORDS

EST.

SOURCE

Homo sapiens

Homo sapiens

ORGANISM

REFERENCE

1 (bases 1 to 955)

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ARCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

BUS38351 955 bp mRNA linear EST 13-SEP-2002  
 AGENCOURT\_10181238 NIH\_MGC\_107 Homo sapiens cDNA clone  
 IMAGE:6568891 5', mRNA sequence.

BUS38351  
 BUS38351.1 GI:22848792  
 EST.  
 Homo sapiens (human)

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 955)

AUTHORS  
 NIH-MGC http://mgi.nci.nih.gov/.

TITLE  
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
 Unpublished

COMMENT  
 Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ARCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be





Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Library constructed by Life Technologies.  
BASE COUNT 201 a 162 c 208 g 152 t  
ORIGIN

Query Match 47.3%; Score 542; DB 10; Length 723;  
Best Local Similarity 100.0%; Pred. No. 1.3e-172; Indels 0; Gaps 0;  
Matches 542; Conservative 0; Mismatches 0;

QY 163 AGATGTTGAACCTGAAGAAGCCTATAGACAGCTGGCAGTGATGGTTTCATCTCGACAAAAA 222  
Db 1 AGATGTTGAACCTGAAGAAGCCTATAGACAGCTGGCAGTGATGGTTTCATCTCGACAAAAA 60

QY 223 TCATCATCCCGGGCTGAGGAGCCTTCAAGGTTTTCGAGCAGCTTGGGACATTGTGAC 282  
Db 61 TCATCATCCCGGGCTGAGGAGCCTTCAAGGTTTTCGAGCAGCTTGGGACATTGTGAC 120

QY 283 CAATGCTGAAAACGCGAAGAGATGATGAGATGAAACGAATGGCAGAGAATGAGTGGCGG 342  
Db 121 CAATGCTGAAAACGCGAAGAGATGATGAGATGAAACGAATGGCAGAGAATGAGTGGCGG 180

QY 343 GTCAGTAAATGAGTTTCTCTCCAGCTGCAAGATGACCTCAAGGAGGCAATGAATACTAT 402  
Db 181 GTCAGTAAATGAGTTTCTCTCCAGCTGCAAGATGACCTCAAGGAGGCAATGAATACTAT 240

QY 403 GATGTTAGCCGATGCCAAGGAAAGCATAGGAGTTTGAATGGACCGGAACTTAAGAG 462  
Db 241 GATGTTAGCCGATGCCAAGGAAAGCATAGGAGTTTGAATGGACCGGAACTTAAGAG 300

QY 463 TGGCAGATAGTGTGCTGAGTGTAATAGGCTGATCTGCTGAGGAGGAGACTTTTGGGC 522  
Db 301 TGGCAGATAGTGTGCTGAGTGTAATAGGCTGATCTGCTGAGGAGGAGACTTTTGGGC 360

QY 523 AGAGTCAAGCATGTTGGGCTCAAGATCACCTACTTTGCACTGATGGATGGAAGGTGTA 582  
Db 361 AGAGTCAAGCATGTTGGGCTCAAGATCACCTACTTTGCACTGATGGATGGAAGGTGTA 420

QY 583 TGACATCACAGAGTGGGCTGGATGCGAGCGTGATGATCTCCCGAGATACCCACAGAGT 642  
Db 421 TGACATCACAGAGTGGGCTGGATGCGAGCGTGATGATCTCCCGAGATACCCACAGAGT 480

QY 643 CCCTATACATCTCAATTTGGTTCTCGGATTCAGGACACAGAGGCGGACAGAGCCAC 702  
Db 481 CCCTATACATCTCAATTTGGTTCTCGGATTCAGGACACAGAGGCGGACAGAGCCAC 540

QY 703 CC 704  
Db 541 CC 542

RESULT 14  
BM424147  
LOCUS  
DEFINITION AGENCOURT\_6398639 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:5517411  
5', mRNA sequence.  
BM424147  
BM424147.1 GI:18392359  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 927)  
NIH-MGC <http://mgi.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LCM2019 row: j column: 04  
High quality sequence stop: 460.  
Location/Qualifiers  
1. 927  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:5517411"  
/tissue\_type="amelanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_41"  
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."  
BASE COUNT 236 a 241 c 245 g 204 t 1 others  
ORIGIN

Query Match 44.4%; Score 509; DB 12; Length 927;  
Best Local Similarity 100.0%; Pred. No. 1.6e-161;  
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 CATCTGACAAAATCATCCCCGGCTCAGGAGGCTTCAGGTTTTCGGAGCAGCT 268  
Db 27 CATCTGACAAAATCATCCCCGGCTCAGGAGGCTTCAGGTTTTCGGAGCAGCT 86

QY 269 TGGGACATTGTGAGCAATGCTGAAAGCGAAAGGAGTATGAGATGAAACGAATGGCAGAG 328  
Db 87 TGGGACATTGTGAGCAATGCTGAAAGCGAAAGGAGTATGAGATGAAACGAATGGCAGAG 146

QY 329 AATGAGCTGAGCCCGTCAAGTAAATGAGTTTCTGCCAAGCTGCAAGATGACCTCAAGGAG 388  
Db 147 AATGAGCTGAGCCCGTCAAGTAAATGAGTTTCTGCCAAGCTGCAAGATGACCTCAAGGAG 206

QY 389 GCAATGAATATCTATGATGTGTAGCCGATGCCAAGAAAGCATAGGAGTTTGAATGGAC 448  
Db 207 GCAATGAATATCTATGATGTGTAGCCGATGCCAAGAAAGCATAGGAGTTTGAATGGAC 266

QY 449 CGGGAACCTAAGAGTGGCAGATCTGTCTGAGTGTAATAGGCTGCATCTCTGCTGAGGAA 508  
Db 267 CGGGAACCTAAGAGTGGCAGATCTGTCTGAGTGTAATAGGCTGCATCTCTGCTGAGGAA 326

QY 509 GGAGACTTTTGGGACAGTCAAGCATGTTGGGCTCAGGATCACTACTTTGCACTGATG 568  
Db 327 GGAGACTTTTGGGACAGTCAAGCATGTTGGGCTCAGGATCACTACTTTGCACTGATG 386

QY 569 GATGAAAGGTGTATGACATCACAGATGGGCTGGATGCCAGCGTGTAGGTATCTCCCA 628  
Db 387 GATGAAAGGTGTATGACATCACAGATGGGCTGGATGCCAGCGTGTAGGTATCTCCCA 446

QY 629 GATACCCACAGATCCCTATCATCTCTATTTGGTTCTCGGATTCAGGACACAGAGGG 688  
Db 447 GATACCCACAGATCCCTATCATCTCTATTTGGTTCTCGGATTCAGGACACAGAGGG 506

QY 689 CGGACAGAGAGCCACCCAGATGCCCTCC 717  
Db 507 CGGACAGAGAGCCACCCAGATGCCCTCC 535

RESULT 15  
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LOCUS  
DEFINITION BG751088 912 bp mRNA linear EST 15-MAY-2001  
602729879F1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:4873555 5', mRNA sequence.  
BG751088  
ACCESSION BG751088  
VERSION BG751088.1 GI:14061741

Db 624 AGGAAAGCATAGGAGGTTTGAATGGACCGGAACCTAAGAGTGCCAGATACTG 677

Search completed: December 22, 2003, 19:59:26  
Job time : 2762 secs

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 912)  
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LCM1751 row: n column: 20  
High quality sequence stop: 778.

FEATURES  
source  
1..912  
Location/Qualifiers  
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/clone="IMAGE:487355"  
/tissue\_type="normal pigmented retinal epithelium"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_43"  
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GCACGAG(G).. Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library. |"

BASE COUNT 225 a 191 c 288 g 208 t

Query Match 41.3%; Score 474; DB 10; Length 912;  
Best Local Similarity 100.0%; Pred. No. 1e-149;  
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTGGGTCAAGCAGAAATTAATAGCGAGGGAATGCACCTGTAGCTAGTGGCGCTA 60  
Db |||||  
204 GCCTTGGGTCAAGCAGAAATTAATAGCGAGGGAATGCACCTGTAGCTAGTGGCGCTA 263  
QY 61 CTGCCAGCCTGAAGAGGAGTGGCTCGACTCTTGACCATGGCTGGGTTCTCTGAGGATGA 120  
Db |||||  
264 CTGCCAGCCTGAAGAGGAGTGGCTCGACTCTTGACCATGGCTGGGTTCTCTGAGGATGA 323  
QY 121 GCTAAACCCCTTCCATGTACTGGGGTTGAGGCCACAGCATCATCTCCCGGGCTGA 180  
Db |||||  
324 GCTAAACCCCTTCCATGTACTGGGGTTGAGGCCACAGCATCATCTCCCGGGCTGA 383  
QY 181 GGCCTATAGCAGCTGGCAGTGTGTTTCATCTCCAGCAAAATCATCTCCCGGGCTGA 240  
Db |||||  
384 GGCCTATAGCAGCTGGCAGTGTGTTTCATCTCCAGCAAAATCATCTCCCGGGCTGA 443  
QY 241 GGAGGCTTCAAGGTTTGGAGCAGCTTGGACATTTGTGACCAATTGTGACCAATGCTGAAAAGCGAAA 300  
Db |||||  
444 GGAGGCTTCAAGGTTTGGAGCAGCTTGGACATTTGTGACCAATTGTGACCAATGCTGAAAAGCGAAA 503  
QY 301 GGAGTATGAGATGAAGCAATGGCAGAGATGAGCTGAGCCGGTCACTAAATGAGTTTCT 360  
Db |||||  
504 GGAGTATGAGATGAAGCAATGGCAGAGATGAGCTGAGCCGGTCACTAAATGAGTTTCT 563  
QY 361 GTCCAAAGCTGCAAGATCACCTCAAGGAGGCAATGAAATGACTATGATGTGTAGCCGATGCCA 420  
Db |||||  
564 GTCCAAAGCTGCAAGATCACCTCAAGGAGGCAATGAAATGACTATGATGTGTAGCCGATGCCA 623  
QY 421 AGGAAAGCATAGGAGGTTTGAATGGACCGGAACCTAAGAGTGCCAGATACTG 474